

# SEQUENCE LISTING

<110> Hardiman, Gerard T.  
 Rock, Fernando L.  
 Bazan, J. Fernando  
 Kastelein, Robert A.  
 Ho, Stephen W.K.  
 Liu, Yong-Jun

<120> Human Receptor Proteins; Related Reagents and Methods

<130> DX0724XK

<140> 09/728,540

<141> 2000-11-28

<160> 45

<170> PatentIn Ver. 2.0

<210> 1

<211> 2367

<212> DNA

<213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>

<221> CDS

<222> (1)..(2358)

<220>

<221> mat\_peptide

<222> (67)..(2358)

<400> 1

atg	act	agc	atc	ttc	cat	ttt	gcc	att	atc	ttc	atg	tta	ata	ctt	cag	48
Met	Thr	Ser	Ile	Phe	His	Phe	Ala	Ile	Ile	Phe	Met	Leu	Ile	Leu	Gln	
							-15								-10	

atc	aga	ata	caa	tta	tct	gaa	gaa	agt	gaa	ttt	tta	gtt	gat	agg	tca	96
Ile	Arg	Ile	Gln	Leu	Ser	Glu	Glu	Ser	Glu	Phe	Leu	Val	Asp	Arg	Ser	
										5					10	

aaa	aac	ggt	ctc	atc	cac	gtt	cct	aaa	gac	cta	tcc	cag	aaa	aca	aca	144
Lys	Asn	Gly	Leu	Ile	His	Val	Pro	Lys	Asp	Leu	Ser	Gln	Lys	Thr	Thr	
				15					20					25		

atc	tta	aat	ata	tcg	caa	aat	tat	ata	tct	gag	ctt	tgg	act	tct	gac	192
Ile	Leu	Asn	Ile	Ser	Gln	Asn	Tyr	Ile	Ser	Glu	Leu	Trp	Thr	Ser	Asp	
				30				35						40		

atc tta tca ctg tca aaa ctg agg att ttg ata att tct cat aat aga	240
Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg	
45 50 55	
atc cag tat ctt gat atc agt gtt ttc aaa ttc aac cag gaa ttg gaa	288
Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu	
60 65 70	
tac ttg gat ttg tcc cac aac aag ttg gtg aag att tct tgc cac cct	336
Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro	
75 80 85 90	
act gtg aac ctc aag cac ttg gac ctg tca ttt aat gca ttt gat gcc	384
Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala	
95 100 105	
ctg cct ata tgc aaa gag ttt ggc aat atg tct caa cta aaa ttt ctg	432
Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu	
110 115 120	
ggg ttg agc acc aca cac tta gaa aaa tct agt gtg ctg cca att gct	480
Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala	
125 130 135	
cat ttg aat atc agc aag gtc ttg ctg gtc tta gga gag act tat ggg	528
His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly	
140 145 150	
gaa aaa gaa gac cct gag ggc ctt caa gac ttt aac act gag agt ctg	576
Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu	
155 160 165 170	
cac att gtg ttc ccc aca aac aaa gaa ttc cat ttt att ttg gat gtg	624
His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val	
175 180 185	
tca gtc aag act gta gca aat ctg gaa cta tct aat atc aaa tgt gtg	672
Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val	
190 195 200	
cta gaa gat aac aaa tgt tct tac ttc cta agt att ctg gcg aaa ctt	720
Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu	
205 210 215	
caa aca aat cca aag tta tca agt ctt acc tta aac aac att gaa aca	768
Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr	
220 225 230	
act tgg aat tct ttc att agg atc ctc caa cta gtt tgg cat aca act	816
Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr	
235 240 245 250	
gta tgg tat ttc tca att tca aac gtg aag cta cag ggt cag ctg gac	864

Val	Trp	Tyr	Phe	Ser	Ile	Ser	Asn	Val	Lys	Leu	Gln	Gly	Gln	Leu	Asp		
				255					260					265			
ttc	aga	gat	ttt	gat	tat	tct	ggc	act	tcc	ttg	aag	gcc	ttg	tct	ata	912	
Phe	Arg	Asp	Phe	Asp	Tyr	Ser	Gly	Thr	Ser	Leu	Lys	Ala	Leu	Ser	Ile		
			270				275						280				
cac	caa	ggt	gtc	agc	gat	gtg	ttc	ggg	ttt	ccg	caa	agt	tat	atc	tat	960	
His	Gln	Val	Val	Ser	Asp	Val	Phe	Gly	Phe	Pro	Gln	Ser	Tyr	Ile	Tyr		
		285					290					295					
gaa	atc	ttt	tcg	aat	atg	aac	atc	aaa	aat	ttc	aca	gtg	tct	ggg	aca	1008	
Glu	Ile	Phe	Ser	Asn	Met	Asn	Ile	Lys	Asn	Phe	Thr	Val	Ser	Gly	Thr		
	300					305					310						
cgc	atg	gtc	cac	atg	ctt	tgc	cca	tcc	aaa	att	agc	ccg	ttc	ctg	cat	1056	
Arg	Met	Val	His	Met	Leu	Cys	Pro	Ser	Lys	Ile	Ser	Pro	Phe	Leu	His		
	315				320					325					330		
ttg	gat	ttt	tcc	aat	aat	ctc	tta	aca	gac	acg	ggt	ttt	gaa	aat	tgt	1104	
Leu	Asp	Phe	Ser	Asn	Asn	Leu	Leu	Thr	Asp	Thr	Val	Phe	Glu	Asn	Cys		
				335					340					345			
ggg	cac	ctt	act	gag	ttg	gag	aca	ctt	att	tta	caa	atg	aat	caa	tta	1152	
Gly	His	Leu	Thr	Glu	Leu	Glu	Thr	Leu	Ile	Leu	Gln	Met	Asn	Gln	Leu		
			350					355					360				
aaa	gaa	ctt	tca	aaa	ata	gct	gaa	atg	act	aca	cag	atg	aag	tct	ctg	1200	
Lys	Glu	Leu	Ser	Lys	Ile	Ala	Glu	Met	Thr	Thr	Gln	Met	Lys	Ser	Leu		
		365					370					375					
caa	caa	ttg	gat	att	agc	cag	aat	tct	gta	agc	tat	gat	gaa	aag	aaa	1248	
Gln	Gln	Leu	Asp	Ile	Ser	Gln	Asn	Ser	Val	Ser	Tyr	Asp	Glu	Lys	Lys		
		380				385					390						
gga	gac	tgt	tct	tgg	act	aaa	agt	tta	tta	agt	tta	aat	atg	tct	tca	1296	
Gly	Asp	Cys	Ser	Trp	Thr	Lys	Ser	Leu	Leu	Ser	Leu	Asn	Met	Ser	Ser		
					400					405					410		
aat	ata	ctt	act	gac	act	att	ttc	aga	tgt	tta	cct	ccc	agg	atc	aag	1344	
Asn	Ile	Leu	Thr	Asp	Thr	Ile	Phe	Arg	Cys	Leu	Pro	Pro	Arg	Ile	Lys		
				415				420						425			
gta	ctt	gat	ctt	cac	agc	aat	aaa	ata	aag	agc	att	cct	aaa	caa	gtc	1392	
Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser	Ile	Pro	Lys	Gln	Val		
			430					435					440				
gta	aaa	ctg	gaa	gct	ttg	caa	gaa	ctc	aat	ggt	gct	ttc	aat	tct	tta	1440	
Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val	Ala	Phe	Asn	Ser	Leu		
		445					450					455					
act	gac	ctt	cct	gga	tgt	ggc	agc	ttt	agc	agc	ctt	tct	gta	ttg	atc	1488	
Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	Ser	Ser	Leu	Ser	Val	Leu	Ile		
		460				465					470						

att gat cac aat tca gtt tcc cac cca tca gct gat ttc ttc cag agc	1536
Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser	
475 480 485 490	
tgc cag aag atg agg tca ata aaa gca ggg gac aat cca ttc caa tgt	1584
Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys	
495 500 505	
acc tgt gag ctc gga gaa ttt gtc aaa aat ata gac caa gta tca agt	1632
Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser	
510 515 520	
gaa gtg tta gag ggc tgg cct gat tct tat aag tgt gac tac ccg gaa	1680
Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu	
525 530 535	
agt tat aga gga acc cta cta aag gac ttt cac atg tct gaa tta tcc	1728
Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser	
540 545 550	
tgc aac ata act ctg ctg atc gtc acc atc gtt gcc acc atg ctg gtg	1776
Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val	
555 560 565 570	
ttg gct gtg act gtg acc tcc ctc tgc atc tac ttg gat ctg ccc tgg	1824
Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp	
575 580 585	
tat ctc agg atg gtg tgc cag tgg acc cag acc cgg cgc agg gcc agg	1872
Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg	
590 595 600	
aac ata ccc tta gaa gaa ctc caa aga aat ctc cag ttt cat gca ttt	1920
Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe	
605 610 615	
att tca tat agt ggg cac gat tct ttc tgg gtg aag aat gaa tta ttg	1968
Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu	
620 625 630	
cca aac cta gag aaa gaa ggt atg cag att tgc ctt cat gag aga aac	2016
Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn	
635 640 645 650	
ttt gtt cct ggc aag agc att gtg gaa aat atc atc acc tgc att gag	2064
Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu	
655 660 665	
aag agt tac aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag agt	2112
Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser	
670 675 680	

gaa tgg tgc cat tat gaa ctc tac ttt gcc cat cac aat ctc ttt cat 2160  
 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His  
 685 690 695

gaa gga tct aat agc tta atc ctg atc ttg ctg gaa ccc att ccg cag 2208  
 Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln  
 700 705 710

tac tcc att cct agc agt tat cac aag ctc aaa agt ctc atg gcc agg 2256  
 Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg  
 715 720 725 730

agg act tat ttg gaa tgg ccc aag gaa aag agc aaa cgt ggc ctt ttt 2304  
 Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe  
 735 740 745

tgg gct aac tta agg gca gcc att aat att aag ctg aca gag caa gca 2352  
 Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala  
 750 755 760

aaa tagtctaga 2367  
 Lys Lys

<210> 2

<211> 786

<212> PRT

<213> Unknown

<400> 2

Met Thr Ser Ile Phe His Phe Ala Ile Ile Phe Met Leu Ile Leu Gln  
 -20 -15 -10

Ile Arg Ile Gln Leu Ser Glu Glu Ser Glu Phe Leu Val Asp Arg Ser  
 -5 -1 1 5 10

Lys Asn Gly Leu Ile His Val Pro Lys Asp Leu Ser Gln Lys Thr Thr  
 15 20 25

Ile Leu Asn Ile Ser Gln Asn Tyr Ile Ser Glu Leu Trp Thr Ser Asp  
 30 35 40

Ile Leu Ser Leu Ser Lys Leu Arg Ile Leu Ile Ile Ser His Asn Arg  
 45 50 55

Ile Gln Tyr Leu Asp Ile Ser Val Phe Lys Phe Asn Gln Glu Leu Glu  
 60 65 70

Tyr Leu Asp Leu Ser His Asn Lys Leu Val Lys Ile Ser Cys His Pro  
 75 80 85 90

Thr Val Asn Leu Lys His Leu Asp Leu Ser Phe Asn Ala Phe Asp Ala  
 95 100 105

Leu Pro Ile Cys Lys Glu Phe Gly Asn Met Ser Gln Leu Lys Phe Leu  
 110 115 120  
 Gly Leu Ser Thr Thr His Leu Glu Lys Ser Ser Val Leu Pro Ile Ala  
 125 130 135  
 His Leu Asn Ile Ser Lys Val Leu Leu Val Leu Gly Glu Thr Tyr Gly  
 140 145 150  
 Glu Lys Glu Asp Pro Glu Gly Leu Gln Asp Phe Asn Thr Glu Ser Leu  
 155 160 165 170  
 His Ile Val Phe Pro Thr Asn Lys Glu Phe His Phe Ile Leu Asp Val  
 175 180 185  
 Ser Val Lys Thr Val Ala Asn Leu Glu Leu Ser Asn Ile Lys Cys Val  
 190 195 200  
 Leu Glu Asp Asn Lys Cys Ser Tyr Phe Leu Ser Ile Leu Ala Lys Leu  
 205 210 215  
 Gln Thr Asn Pro Lys Leu Ser Ser Leu Thr Leu Asn Asn Ile Glu Thr  
 220 225 230  
 Thr Trp Asn Ser Phe Ile Arg Ile Leu Gln Leu Val Trp His Thr Thr  
 235 240 245 250  
 Val Trp Tyr Phe Ser Ile Ser Asn Val Lys Leu Gln Gly Gln Leu Asp  
 255 260 265  
 Phe Arg Asp Phe Asp Tyr Ser Gly Thr Ser Leu Lys Ala Leu Ser Ile  
 270 275 280  
 His Gln Val Val Ser Asp Val Phe Gly Phe Pro Gln Ser Tyr Ile Tyr  
 285 290 295  
 Glu Ile Phe Ser Asn Met Asn Ile Lys Asn Phe Thr Val Ser Gly Thr  
 300 305 310  
 Arg Met Val His Met Leu Cys Pro Ser Lys Ile Ser Pro Phe Leu His  
 315 320 325 330  
 Leu Asp Phe Ser Asn Asn Leu Leu Thr Asp Thr Val Phe Glu Asn Cys  
 335 340 345  
 Gly His Leu Thr Glu Leu Glu Thr Leu Ile Leu Gln Met Asn Gln Leu  
 350 355 360  
 Lys Glu Leu Ser Lys Ile Ala Glu Met Thr Thr Gln Met Lys Ser Leu  
 365 370 375  
 Gln Gln Leu Asp Ile Ser Gln Asn Ser Val Ser Tyr Asp Glu Lys Lys  
 380 385 390

Gly Asp Cys Ser Trp Thr Lys Ser Leu Leu Ser Leu Asn Met Ser Ser  
 395 400 405 410  
 Asn Ile Leu Thr Asp Thr Ile Phe Arg Cys Leu Pro Pro Arg Ile Lys  
 415 420 425  
 Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser Ile Pro Lys Gln Val  
 430 435 440  
 Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val Ala Phe Asn Ser Leu  
 445 450 455  
 Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser Leu Ser Val Leu Ile  
 460 465 470  
 Ile Asp His Asn Ser Val Ser His Pro Ser Ala Asp Phe Phe Gln Ser  
 475 480 485 490  
 Cys Gln Lys Met Arg Ser Ile Lys Ala Gly Asp Asn Pro Phe Gln Cys  
 495 500 505  
 Thr Cys Glu Leu Gly Glu Phe Val Lys Asn Ile Asp Gln Val Ser Ser  
 510 515 520  
 Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys Cys Asp Tyr Pro Glu  
 525 530 535  
 Ser Tyr Arg Gly Thr Leu Leu Lys Asp Phe His Met Ser Glu Leu Ser  
 540 545 550  
 Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Val Ala Thr Met Leu Val  
 555 560 565 570  
 Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr Leu Asp Leu Pro Trp  
 575 580 585  
 Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr Arg Arg Arg Ala Arg  
 590 595 600  
 Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe  
 605 610 615  
 Ile Ser Tyr Ser Gly His Asp Ser Phe Trp Val Lys Asn Glu Leu Leu  
 620 625 630  
 Pro Asn Leu Glu Lys Glu Gly Met Gln Ile Cys Leu His Glu Arg Asn  
 635 640 645 650  
 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Thr Cys Ile Glu  
 655 660 665  
 Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser  
 670 675 680

Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His  
685 690 695

Glu Gly Ser Asn Ser Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln  
700 705 710

Tyr Ser Ile Pro Ser Ser Tyr His Lys Leu Lys Ser Leu Met Ala Arg  
715 720 725 730

Arg Thr Tyr Leu Glu Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe  
735 740 745

Trp Ala Asn Leu Arg Ala Ala Ile Asn Ile Lys Leu Thr Glu Gln Ala  
750 755 760

Lys Lys

<210> 3

<211> 2355

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(2352)

<220>

<221> mat\_peptide

<222> (67)..(2352)

<400> 3

atg cca cat act ttg tgg atg gtg tgg gtc ttg ggg gtc atc atc agc 48  
Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser  
-20 -15 -10

ctc tcc aag gaa gaa tcc tcc aat cag gct tct ctg tct tgt gac cgc 96  
Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg  
-5 -1 1 5 10

aat ggt atc tgc aag ggc agc tca gga tct tta aac tcc att ccc tca 144  
Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser  
15 20 25

ggg ctc aca gaa gct gta aaa agc ctt gac ctg tcc aac aac agg atc 192  
Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile  
30 35 40



acc tac att agc aac agt gac cta cag agg tgt gtg aac ctc cag gct	240
Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala	
45 50 55	
ctg gtg ctg aca tcc aat gga att aac aca ata gag gaa gat tct ttt	288
Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe	
60 65 70	
tct tcc ctg ggc agt ctt gaa cat tta gac tta tcc tat aat tac tta	336
Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu	
75 80 85 90	
tct aat tta tct tct tcc tgg ttc aag ccc ctt tct tct tta aca ttc	384
Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe	
95 100 105	
tta aac tta ctg gga aat cct tac aaa acc cta ggg gaa aca tct ctt	432
Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu	
110 115 120	
tct cat ctc aca aaa ttg caa atc ctg aga gtg gga aat atg gac	480
Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp	
125 130 135	
acc ttc act aag att caa aga aaa gat ttt gct gga ctt acc ttc ctt	528
Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu	
140 145 150	
gag gaa ctt gag att gat gct tca gat cta cag agc tat gag cca aaa	576
Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys	
155 160 165 170	
agt ttg aag tca att cag aac gta agt cat ctg atc ctt cat atg aag	624
Ser Leu Lys Ser Ile Gln Asn Val Ser His Leu Ile Leu His Met Lys	
175 180 185	
cag cat att tta ctg ctg gag att ttt gta gat gtt aca agt tcc gtg	672
Gln His Ile Leu Leu Leu Glu Ile Phe Val Asp Val Thr Ser Ser Val	
190 195 200	
gaa tgt ttg gaa ctg cga gat act gat ttg gac act ttc cat ttt tca	720
Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser	
205 210 215	
gaa cta tcc act ggt gaa aca aat tca ttg att aaa aag ttt aca ttt	768
Glu Leu Ser Thr Gly Glu Thr Asn Ser Leu Ile Lys Lys Phe Thr Phe	
220 225 230	
aga aat gtg aaa atc acc gat gaa agt ttg ttt cag gtt atg aaa ctt	816
Arg Asn Val Lys Ile Thr Asp Glu Ser Leu Phe Gln Val Met Lys Leu	
235 240 245 250	
ttg aat cag att tct gga ttg tta gaa tta gag ttt gat gac tgt acc	864

Leu	Asn	Gln	Ile	Ser	Gly	Leu	Leu	Glu	Leu	Glu	Phe	Asp	Asp	Cys	Thr		
				255					260					265			
ctt	aat	gga	gtt	ggt	aat	ttt	aga	gca	tct	gat	aat	gac	aga	gtt	ata	912	
Leu	Asn	Gly	Val	Gly	Asn	Phe	Arg	Ala	Ser	Asp	Asn	Asp	Arg	Val	Ile		
			270					275					280				
gat	cca	ggt	aaa	gtg	gaa	acg	tta	aca	atc	cgg	agg	ctg	cat	att	cca	960	
Asp	Pro	Gly	Lys	Val	Glu	Thr	Leu	Thr	Ile	Arg	Arg	Leu	His	Ile	Pro		
			285				290					295					
agg	ttt	tac	tta	ttt	tat	gat	ctg	agc	act	tta	tat	tca	ctt	aca	gaa	1008	
Arg	Phe	Tyr	Leu	Phe	Tyr	Asp	Leu	Ser	Thr	Leu	Tyr	Ser	Leu	Thr	Glu		
	300					305					310						
aga	gtt	aaa	aga	atc	aca	gta	gaa	aac	agt	aaa	gtt	ttt	ctg	gtt	cct	1056	
Arg	Val	Lys	Arg	Ile	Thr	Val	Glu	Asn	Ser	Lys	Val	Phe	Leu	Val	Pro		
	315				320					325					330		
tgt	tta	ctt	tca	caa	cat	tta	aaa	tca	tta	gaa	tac	ttg	gat	ctc	agt	1104	
Cys	Leu	Leu	Ser	Gln	His	Leu	Lys	Ser	Leu	Glu	Tyr	Leu	Asp	Leu	Ser		
				335					340					345			
gaa	aat	ttg	atg	gtt	gaa	gaa	tac	ttg	aaa	aat	tca	gcc	tgt	gag	gat	1152	
Glu	Asn	Leu	Met	Val	Glu	Glu	Tyr	Leu	Lys	Asn	Ser	Ala	Cys	Glu	Asp		
			350					355					360				
gcc	tgg	ccc	tct	cta	caa	act	tta	att	tta	agg	caa	aat	cat	ttg	gca	1200	
Ala	Trp	Pro	Ser	Leu	Gln	Thr	Leu	Ile	Leu	Arg	Gln	Asn	His	Leu	Ala		
			365				370					375					
tca	ttg	gaa	aaa	acc	gga	gag	act	ttg	ctc	act	ctg	aaa	aac	ttg	act	1248	
Ser	Leu	Glu	Lys	Thr	Gly	Glu	Thr	Leu	Leu	Thr	Leu	Lys	Asn	Leu	Thr		
	380					385					390						
aac	att	gat	atc	agt	aag	aat	agt	ttt	cat	tct	atg	cct	gaa	act	tgt	1296	
Asn	Ile	Asp	Ile	Ser	Lys	Asn	Ser	Phe	His	Ser	Met	Pro	Glu	Thr	Cys		
					400					405					410		
cag	tgg	cca	gaa	aag	atg	aaa	tat	ttg	aac	tta	tcc	agc	aca	cga	ata	1344	
Gln	Trp	Pro	Glu	Lys	Met	Lys	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Arg	Ile		
				415					420					425			
cac	agt	gta	aca	ggc	tgc	att	ccc	aag	aca	ctg	gaa	att	tta	gat	gtt	1392	
His	Ser	Val	Thr	Gly	Cys	Ile	Pro	Lys	Thr	Leu	Glu	Ile	Leu	Asp	Val		
			430					435					440				
agc	aac	aac	aat	ctc	aat	tta	ttt	tct	ttg	aat	ttg	ccg	caa	ctc	aaa	1440	
Ser	Asn	Asn	Asn	Leu	Asn	Leu	Phe	Ser	Leu	Asn	Leu	Pro	Gln	Leu	Lys		
			445				450					455					
gaa	ctt	tat	att	tcc	aga	aat	aag	ttg	atg	act	cta	cca	gat	gcc	tcc	1488	
Glu	Leu	Tyr	Ile	Ser	Arg	Asn	Lys	Leu	Met	Thr	Leu	Pro	Asp	Ala	Ser		

460	465	470	
ctc tta ccc atg tta cta gta ttg aaa atc agt agg aat gca ata act Leu Leu Pro Met Leu Leu Val Leu Lys Ile Ser Arg Asn Ala Ile Thr 475 480 485 490			1536
acg ttt tct aag gag caa ctt gac tca ttt cac aca ctg aag act ttg Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu 495 500 505			1584
gaa gct ggt ggc aat aac ttc att tgc tcc tgt gaa ttc ctc tcc ttc Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe 510 515 520			1632
act cag gag cag caa gca ctg gcc aaa gtc ttg att gat tgg cca gca Thr Gln Glu Gln Gln Ala Leu Ala Lys Val Leu Ile Asp Trp Pro Ala 525 530 535			1680
aat tac ctg tgt gac tct cca tcc cat gtg cgt ggc cag cag gtt cag Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln 540 545 550			1728
gat gtc cgc ctc tcg gtg tcg gaa tgt cac agg aca gca ctg gtg tct Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser 555 560 565 570			1776
ggc atg tgc tgt gct ctg ttc ctg ctg atc ctg ctc acg ggg gtc ctg Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu 575 580 585			1824
tgc cac cgt ttc cat ggc ctg tgg tat atg aaa atg atg tgg gcc tgg Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp 590 595 600			1872
ctc cag gcc aaa agg aag ccc agg aaa gct ccc agc agg aac atc tgc Leu Gln Ala Lys Arg Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys 605 610 615			1920
tat gat gca ttt gtt tct tac agt gag cgg gat gcc tac tgg gtg gag Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu 620 625 630			1968
aac ctt atg gtc cag gag ctg gag aac ttc aat ccc ccc ttc aag ttg Asn Leu Met Val Gln Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu 635 640 645 650			2016
tgt ctt cat aag cgg gac ttc att cct ggc aag tgg atc att gac aat Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn 655 660 665			2064
atc att gac tcc att gaa aag agc cac aaa act gtc ttt gtg ctt tct Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser 670 675 680			2112

gaa aac ttt gtg aag agt gag tgg tgc aag tat gaa ctg gac ttc tcc 2160  
 Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser  
 685 690 695

cat ttc cgt ctt ttt gaa gag aac aat gat gct gcc att ctc att ctt 2208  
 His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu  
 700 705 710

ctg gag ccc att gag aaa aaa gcc att ccc cag cgc ttc tgc aag ctg 2256  
 Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu  
 715 720 725 730

cgg aag ata atg aac acc aag acc tac ctg gag tgg ccc atg gac gag 2304  
 Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu  
 735 740 745

gct cag cgg gaa gga ttt tgg gta aat ctg aga gct gcg ata aag tcc 2352  
 Ala Gln Arg Glu Gly Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser  
 750 755 760

tag 2355

<210> 4  
 <211> 784  
 <212> PRT  
 <213> Unknown

<400> 4  
 Met Pro His Thr Leu Trp Met Val Trp Val Leu Gly Val Ile Ile Ser  
 -20 -15 -10

Leu Ser Lys Glu Glu Ser Ser Asn Gln Ala Ser Leu Ser Cys Asp Arg  
 -5 -1 1 5 10

Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser  
 15 20 25

Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile  
 30 35 40

Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala  
 45 50 55

Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe  
 60 65 70

Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu  
 75 80 85 90

Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe  
 95 100 105

Leu Asn Leu Leu Gly Asn Pro Tyr Lys Thr Leu Gly Glu Thr Ser Leu  
 110 115 120

Phe Ser His Leu Thr Lys Leu Gln Ile Leu Arg Val Gly Asn Met Asp  
 125 130 135

Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu  
 140 145 150

Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys  
 155 160 165 170

Ser Leu Lys Ser Ile Gln Asn Val Ser His Leu Ile Leu His Met Lys  
 175 180 185

Gln His Ile Leu Leu Leu Glu Ile Phe Val Asp Val Thr Ser Ser Val  
 190 195 200

Glu Cys Leu Glu Leu Arg Asp Thr Asp Leu Asp Thr Phe His Phe Ser  
 205 210 215

Glu Leu Ser Thr Gly Glu Thr Asn Ser Leu Ile Lys Lys Phe Thr Phe  
 220 225 230

Arg Asn Val Lys Ile Thr Asp Glu Ser Leu Phe Gln Val Met Lys Leu  
 235 240 245 250

Leu Asn Gln Ile Ser Gly Leu Leu Glu Leu Glu Phe Asp Asp Cys Thr  
 255 260 265

Leu Asn Gly Val Gly Asn Phe Arg Ala Ser Asp Asn Asp Arg Val Ile  
 270 275 280

Asp Pro Gly Lys Val Glu Thr Leu Thr Ile Arg Arg Leu His Ile Pro  
 285 290 295

Arg Phe Tyr Leu Phe Tyr Asp Leu Ser Thr Leu Tyr Ser Leu Thr Glu  
 300 305 310

Arg Val Lys Arg Ile Thr Val Glu Asn Ser Lys Val Phe Leu Val Pro  
 315 320 325 330

Cys Leu Leu Ser Gln His Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser  
 335 340 345

Glu Asn Leu Met Val Glu Glu Tyr Leu Lys Asn Ser Ala Cys Glu Asp  
 350 355 360

Ala Trp Pro Ser Leu Gln Thr Leu Ile Leu Arg Gln Asn His Leu Ala  
 365 370 375

Ser Leu Glu Lys Thr Gly Glu Thr Leu Leu Thr Leu Lys Asn Leu Thr  
 380 385 390

Asn Ile Asp Ile Ser Lys Asn Ser Phe His Ser Met Pro Glu Thr Cys  
 395 400 405 410  
 Gln Trp Pro Glu Lys Met Lys Tyr Leu Asn Leu Ser Ser Thr Arg Ile  
 415 420 425  
 His Ser Val Thr Gly Cys Ile Pro Lys Thr Leu Glu Ile Leu Asp Val  
 430 435 440  
 Ser Asn Asn Asn Leu Asn Leu Phe Ser Leu Asn Leu Pro Gln Leu Lys  
 445 450 455  
 Glu Leu Tyr Ile Ser Arg Asn Lys Leu Met Thr Leu Pro Asp Ala Ser  
 460 465 470  
 Leu Leu Pro Met Leu Leu Val Leu Lys Ile Ser Arg Asn Ala Ile Thr  
 475 480 485 490  
 Thr Phe Ser Lys Glu Gln Leu Asp Ser Phe His Thr Leu Lys Thr Leu  
 495 500 505  
 Glu Ala Gly Gly Asn Asn Phe Ile Cys Ser Cys Glu Phe Leu Ser Phe  
 510 515 520  
 Thr Gln Glu Gln Gln Ala Leu Ala Lys Val Leu Ile Asp Trp Pro Ala  
 525 530 535  
 Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln  
 540 545 550  
 Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser  
 555 560 565 570  
 Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu  
 575 580 585  
 Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp  
 590 595 600  
 Leu Gln Ala Lys Arg Lys Pro Arg Lys Ala Pro Ser Arg Asn Ile Cys  
 605 610 615  
 Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu  
 620 625 630  
 Asn Leu Met Val Gln Glu Leu Glu Asn Phe Asn Pro Pro Phe Lys Leu  
 635 640 645 650  
 Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn  
 655 660 665  
 Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser  
 670 675 680

Glu Asn Phe Val Lys Ser Glu Trp Cys Lys Tyr Glu Leu Asp Phe Ser  
685 690 695

His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu  
700 705 710

Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu  
715 720 725 730

Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu  
735 740 745

Ala Gln Arg Glu Gly Phe Trp Val Asn Leu Arg Ala Ala Ile Lys Ser  
750 755 760

<210> 5

<211> 2715

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(2712)

<220>

<221> mat\_peptide

<222> (64)..(2712)

<400> 5

atg aga cag act ttg cct tgt atc tac ttt tgg ggg ggc ctt ttg ccc 48  
Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro  
-20 -15 -10

ttt ggg atg ctg tgt gca tcc tcc acc acc aag tgc act gtt agc cat 96  
Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His  
-5 -1 1 5 10

gaa gtt gct gac tgc agc cac ctg aag ttg act cag gta ccc gat gat 144  
Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp  
15 20 25

cta ccc aca aac ata aca gtg ttg aac ctt acc cat aat caa ctc aga 192  
Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg  
30 35 40

aga tta cca gcc gcc aac ttc aca agg tat agc cag cta act agc ttg 240  
Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu  
45 50 55

gat gta gga ttt aac acc atc tca aaa ctg gag cca gaa ttg tgc cag	288
Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu Pro Glu Leu Cys Gln	
60 65 70 75	
aaa ctt ccc atg tta aaa gtt ttg aac ctc gag cac aat gag cta tct	336
Lys Leu Pro Met Leu Lys Val Leu Asn Leu Gln His Asn Glu Leu Ser	
80 85 90	
caa ctt tct gat aaa acc ttt gcc ttc tgc acg aat ttg act gaa ctc	384
Gln Leu Ser Asp Lys Thr Phe Ala Phe Cys Thr Asn Leu Thr Glu Leu	
95 100 105	
cat ctc atg tcc aac tca atc cag aaa att aaa aat aat ccc ttt gtc	432
His Leu Met Ser Asn Ser Ile Gln Lys Ile Lys Asn Asn Pro Phe Val	
110 115 120	
aag cag aag aat tta atc aca tta gat ctg tct cat aat ggc ttg tca	480
Lys Gln Lys Asn Leu Ile Thr Leu Asp Leu Ser His Asn Gly Leu Ser	
125 130 135	
tct aca aaa tta gga act cag gtt cag ctg gaa aat ctc caa gag ctt	528
Ser Thr Lys Leu Gly Thr Gln Val Gln Leu Glu Asn Leu Gln Glu Leu	
140 145 150 155	
cta tta tca aac aat aaa att caa gcg cta aaa agt gaa gaa ctg gat	576
Leu Leu Ser Asn Asn Lys Ile Gln Ala Leu Lys Ser Glu Glu Leu Asp	
160 165 170	
att ttt gcc aat tca tct tta aaa aaa tta gag ttg tca tcg aat caa	624
Ile Phe Ala Asn Ser Ser Leu Lys Lys Leu Glu Leu Ser Ser Asn Gln	
175 180 185	
att aaa gag ttt tct cca ggg tgt ttt cac gca att gga aga tta ttt	672
Ile Lys Glu Phe Ser Pro Gly Cys Phe His Ala Ile Gly Arg Leu Phe	
190 195 200	
ggc ctc ttt ctg aac aat gtc cag ctg ggt ccc agc ctt aca gag aag	720
Gly Leu Phe Leu Asn Asn Val Gln Leu Gly Pro Ser Leu Thr Glu Lys	
205 210 215	
cta tgt ttg gaa tta gca aac aca agc att cgg aat ctg tct ctg agt	768
Leu Cys Leu Glu Leu Ala Asn Thr Ser Ile Arg Asn Leu Ser Leu Ser	
220 225 230 235	
aac agc cag ctg tcc acc acc agc aat aca act ttc ttg gga cta aag	816
Asn Ser Gln Leu Ser Thr Thr Ser Asn Thr Thr Phe Leu Gly Leu Lys	
240 245 250	
tgg aca aat ctc act atg ctc gat ctt tcc tac aac aac tta aat gtg	864
Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val	
255 260 265	



gtt ggt aac gat tcc ttt gct tgg ctt cca caa cta gaa tat ttc ttc	912
Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe	
270 275 280	
cta gag tat aat aat ata cag cat ttg ttt tct cac tct ttg cac ggg	960
Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly	
285 290 295	
ctt ttc aat gtg agg tac ctg aat ttg aaa cgg tct ttt act aaa caa	1008
Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln	
300 305 310 315	
agt att tcc ctt gcc tca ctc ccc aag att gat gat ttt tct ttt cag	1056
Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln	
320 325 330	
tgg cta aaa tgt ttg gag cac ctt aac atg gaa gat aat gat att cca	1104
Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro	
335 340 345	
ggc ata aaa agc aat atg ttc aca gga ttg ata aac ctg aaa tac tta	1152
Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu	
350 355 360	
agg cta tcc aac tcc ttt aca agt ttg cga act ttg aca aat gaa aca	1200
Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr	
365 370 375	
ttt gta tca ctt gct cat tct ccc tta cac ata ctc aac cta acc aag	1248
Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys	
380 385 390 395	
aat aaa atc tca aaa ata gag agt gat gct ttc tct tgg ttg ggc cac	1296
Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His	
400 405 410	
cta gaa gta ctt gac ctg ggc ctt aat gaa att ggg caa gaa ctc aca	1344
Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr	
415 420 425	
ggc cag gaa tgg aga ggt cta gaa aat att ttc gaa atc tat ctt tcc	1392
Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser	
430 435 440	
tac aac aag tac ctg cag ctg act agg aac tcc ttt gcc ttg gtc cca	1440
Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro	
445 450 455	
agc ctt caa cga ctg atg ctc cga agg gtg gcc ctt aaa aat gtg gat	1488
Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp	
460 465 470 475	
agc tct cct tca cca ttc cag cct ctt cgt aac ttg acc att ctg gat	1536
Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp	

480										485					490					
cta	agc	aac	aac	aac	ata	gcc	aac	ata	aat	gat	gac	atg	ttg	gag	ggg	1584				
Leu	Ser	Asn	Asn	Asn	Ile	Ala	Asn	Ile	Asn	Asp	Asp	Met	Leu	Glu	Gly					
		495						500					505							
ctt	gag	aaa	cta	gaa	att	ctc	gat	ttg	cag	cat	aac	aac	tta	gca	cgg	1632				
Leu	Glu	Lys	Leu	Glu	Ile	Leu	Asp	Leu	Gln	His	Asn	Asn	Leu	Ala	Arg					
		510					515					520								
ctc	tgg	aaa	cac	gca	aac	cct	ggg	ggg	ccc	att	tat	ttc	cta	aag	ggg	1680				
Leu	Trp	Lys	His	Ala	Asn	Pro	Gly	Gly	Pro	Ile	Tyr	Phe	Leu	Lys	Gly					
		525				530					535									
ctg	tct	cac	ctc	cac	atc	ctt	aac	ttg	gag	tcc	aac	ggc	ttt	gac	gag	1728				
Leu	Ser	His	Leu	His	Ile	Leu	Asn	Leu	Glu	Ser	Asn	Gly	Phe	Asp	Glu					
					545					550					555					
atc	cca	gtt	gag	gtc	ttc	aag	gat	tta	ttt	gaa	cta	aag	atc	atc	gat	1776				
Ile	Pro	Val	Glu	Val	Phe	Lys	Asp	Leu	Phe	Glu	Leu	Lys	Ile	Ile	Asp					
				560					565					570						
tta	gga	ttg	aat	aat	tta	aac	aca	ctt	cca	gca	tct	gtc	ttt	aat	aat	1824				
Leu	Gly	Leu	Asn	Asn	Leu	Asn	Thr	Leu	Pro	Ala	Ser	Val	Phe	Asn	Asn					
			575					580					585							
cag	gtg	tct	cta	aag	tca	ttg	aac	ctt	cag	aag	aat	ctc	ata	aca	tcc	1872				
Gln	Val	Ser	Leu	Lys	Ser	Leu	Asn	Leu	Gln	Lys	Asn	Leu	Ile	Thr	Ser					
		590					595					600								
ggt	gag	aag	aag	gtt	ttc	ggg	cca	gct	ttc	agg	aac	ctg	act	gag	tta	1920				
Val	Glu	Lys	Lys	Val	Phe	Gly	Pro	Ala	Phe	Arg	Asn	Leu	Thr	Glu	Leu					
		605				610					615									
ggt	atg	cgc	ttt	aat	ccc	ttt	gat	tgc	acg	tgt	gaa	agt	att	gcc	tgg	1968				
Asp	Met	Arg	Phe	Asn	Pro	Phe	Asp	Cys	Thr	Cys	Glu	Ser	Ile	Ala	Trp					
					625					630					635					
ttt	gtt	aat	tgg	att	aac	gag	acc	cat	acc	aac	atc	cct	gag	ctg	tca	2016				
Phe	Val	Asn	Trp	Ile	Asn	Glu	Thr	His	Thr	Asn	Ile	Pro	Glu	Leu	Ser					
				640					645					650						
agc	cac	tac	ctt	tgc	aac	act	cca	cct	cac	tat	cat	ggg	ttc	cca	gtg	2064				
Ser	His	Tyr	Leu	Cys	Asn	Thr	Pro	Pro	His	Tyr	His	Gly	Phe	Pro	Val					
			655					660					665							
aga	ctt	ttt	gat	aca	tca	tct	tgc	aaa	gac	agt	gcc	ccc	ttt	gaa	ctc	2112				
Arg	Leu	Phe	Asp	Thr	Ser	Ser	Cys	Lys	Asp	Ser	Ala	Pro	Phe	Glu	Leu					
		670					675					680								
ttt	ttc	atg	atc	aat	acc	agt	atc	ctg	ttg	att	ttt	atc	ttt	att	gta	2160				
Phe	Phe	Met	Ile	Asn	Thr	Ser	Ile	Leu	Leu	Ile	Phe	Ile	Phe	Ile	Val					
		685				690					695									

ctt ctc atc cac ttt gag ggc tgg agg ata tct ttt tat tgg aat gtt	2208
Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val	
700 705 710 715	
tca gta cat cga gtt ctt ggt ttc aaa gaa ata gac aga cag aca gaa	2256
Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu	
720 725 730	
cag ttt gaa tat gca gca tat ata att cat gcc tat aaa gat aag gat	2304
Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp	
735 740 745	
tgg gtc tgg gaa cat ttc tct tca atg gaa aag gaa gac caa tct ctc	2352
Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu	
750 755 760	
aaa ttt tgt ctg gaa gaa agg gac ttt gag gcg ggt gtt ttt gaa cta	2400
Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu	
765 770 775	
gaa gca att gtt aac agc atc aaa aga agc aga aaa att att ttt gtt	2448
Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val	
780 785 790 795	
aca cac cat cta tta aaa gac cca tta tgc aaa aga ttc aag gta	2496
Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val	
800 805 810	
cat cat gca gtt caa caa gct att gaa caa aat ctg gat tcc att ata	2544
His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile	
815 820 825	
tgg gtt ttc ctt gag gag att cca gat tat aaa ctg aac cat gca ctc	2592
Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu	
830 835 840	
tgt ttg cga aga gga atg ttt aaa tct cac tgc atc ttg aac tgg cca	2640
Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro	
845 850 855	
gtt cag aaa gaa cgg ata ggt gcc ttt cgt cat aaa ttg caa gta gca	2688
Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala	
860 865 870 875	
ctt gga tcc aaa aac tct gta cat taa	2715
Leu Gly Ser Lys Asn Ser Val His	
880	

<210> 6

<211> 904

<212> PRT

<213> Unknown

<400> 6

Met	Arg	Gln	Thr	Leu	Pro	Cys	Ile	Tyr	Phe	Trp	Gly	Gly	Leu	Leu	Pro		
	-20					-15					-10						
Phe	Gly	Met	Leu	Cys	Ala	Ser	Ser	Thr	Thr	Lys	Cys	Thr	Val	Ser	His		
-5				-1	1				5					10			
Glu	Val	Ala	Asp	Cys	Ser	His	Leu	Lys	Leu	Thr	Gln	Val	Pro	Asp	Asp		
			15					20					25				
Leu	Pro	Thr	Asn	Ile	Thr	Val	Leu	Asn	Leu	Thr	His	Asn	Gln	Leu	Arg		
		30					35					40					
Arg	Leu	Pro	Ala	Ala	Asn	Phe	Thr	Arg	Tyr	Ser	Gln	Leu	Thr	Ser	Leu		
	45					50					55						
Asp	Val	Gly	Phe	Asn	Thr	Ile	Ser	Lys	Leu	Glu	Pro	Glu	Leu	Cys	Gln		
60					65					70					75		
Lys	Leu	Pro	Met	Leu	Lys	Val	Leu	Asn	Leu	Gln	His	Asn	Glu	Leu	Ser		
				80					85						90		
Gln	Leu	Ser	Asp	Lys	Thr	Phe	Ala	Phe	Cys	Thr	Asn	Leu	Thr	Glu	Leu		
			95					100					105				
His	Leu	Met	Ser	Asn	Ser	Ile	Gln	Lys	Ile	Lys	Asn	Asn	Pro	Phe	Val		
		110					115					120					
Lys	Gln	Lys	Asn	Leu	Ile	Thr	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu	Ser		
	125					130					135						
Ser	Thr	Lys	Leu	Gly	Thr	Gln	Val	Gln	Leu	Glu	Asn	Leu	Gln	Glu	Leu		
140					145					150					155		
Leu	Leu	Ser	Asn	Asn	Lys	Ile	Gln	Ala	Leu	Lys	Ser	Glu	Glu	Leu	Asp		
				160					165					170			
Ile	Phe	Ala	Asn	Ser	Ser	Leu	Lys	Lys	Leu	Glu	Leu	Ser	Ser	Asn	Gln		
			175					180					185				
Ile	Lys	Glu	Phe	Ser	Pro	Gly	Cys	Phe	His	Ala	Ile	Gly	Arg	Leu	Phe		
	190						195					200					
Gly	Leu	Phe	Leu	Asn	Asn	Val	Gln	Leu	Gly	Pro	Ser	Leu	Thr	Glu	Lys		
	205					210					215						
Leu	Cys	Leu	Glu	Leu	Ala	Asn	Thr	Ser	Ile	Arg	Asn	Leu	Ser	Leu	Ser		
220					225					230					235		
Asn	Ser	Gln	Leu	Ser	Thr	Thr	Ser	Asn	Thr	Thr	Phe	Leu	Gly	Leu	Lys		
				240					245					250			

Trp Thr Asn Leu Thr Met Leu Asp Leu Ser Tyr Asn Asn Leu Asn Val  
 255 260 265  
 Val Gly Asn Asp Ser Phe Ala Trp Leu Pro Gln Leu Glu Tyr Phe Phe  
 270 275 280  
 Leu Glu Tyr Asn Asn Ile Gln His Leu Phe Ser His Ser Leu His Gly  
 285 290 295  
 Leu Phe Asn Val Arg Tyr Leu Asn Leu Lys Arg Ser Phe Thr Lys Gln  
 300 305 310 315  
 Ser Ile Ser Leu Ala Ser Leu Pro Lys Ile Asp Asp Phe Ser Phe Gln  
 320 325 330  
 Trp Leu Lys Cys Leu Glu His Leu Asn Met Glu Asp Asn Asp Ile Pro  
 335 340 345  
 Gly Ile Lys Ser Asn Met Phe Thr Gly Leu Ile Asn Leu Lys Tyr Leu  
 350 355 360  
 Ser Leu Ser Asn Ser Phe Thr Ser Leu Arg Thr Leu Thr Asn Glu Thr  
 365 370 375  
 Phe Val Ser Leu Ala His Ser Pro Leu His Ile Leu Asn Leu Thr Lys  
 380 385 390 395  
 Asn Lys Ile Ser Lys Ile Glu Ser Asp Ala Phe Ser Trp Leu Gly His  
 400 405 410  
 Leu Glu Val Leu Asp Leu Gly Leu Asn Glu Ile Gly Gln Glu Leu Thr  
 415 420 425  
 Gly Gln Glu Trp Arg Gly Leu Glu Asn Ile Phe Glu Ile Tyr Leu Ser  
 430 435 440  
 Tyr Asn Lys Tyr Leu Gln Leu Thr Arg Asn Ser Phe Ala Leu Val Pro  
 445 450 455  
 Ser Leu Gln Arg Leu Met Leu Arg Arg Val Ala Leu Lys Asn Val Asp  
 460 465 470 475  
 Ser Ser Pro Ser Pro Phe Gln Pro Leu Arg Asn Leu Thr Ile Leu Asp  
 480 485 490  
 Leu Ser Asn Asn Asn Ile Ala Asn Ile Asn Asp Asp Met Leu Glu Gly  
 495 500 505  
 Leu Glu Lys Leu Glu Ile Leu Asp Leu Gln His Asn Asn Leu Ala Arg  
 510 515 520  
 Leu Trp Lys His Ala Asn Pro Gly Gly Pro Ile Tyr Phe Leu Lys Gly  
 525 530 535

Leu Ser His Leu His Ile Leu Asn Leu Glu Ser Asn Gly Phe Asp Glu  
 540 545 550 555  
 Ile Pro Val Glu Val Phe Lys Asp Leu Phe Glu Leu Lys Ile Ile Asp  
 560 565 570  
 Leu Gly Leu Asn Asn Leu Asn Thr Leu Pro Ala Ser Val Phe Asn Asn  
 575 580 585  
 Gln Val Ser Leu Lys Ser Leu Asn Leu Gln Lys Asn Leu Ile Thr Ser  
 590 595 600  
 Val Glu Lys Lys Val Phe Gly Pro Ala Phe Arg Asn Leu Thr Glu Leu  
 605 610 615  
 Asp Met Arg Phe Asn Pro Phe Asp Cys Thr Cys Glu Ser Ile Ala Trp  
 620 625 630 635  
 Phe Val Asn Trp Ile Asn Glu Thr His Thr Asn Ile Pro Glu Leu Ser  
 640 645 650  
 Ser His Tyr Leu Cys Asn Thr Pro Pro His Tyr His Gly Phe Pro Val  
 655 660 665  
 Arg Leu Phe Asp Thr Ser Ser Cys Lys Asp Ser Ala Pro Phe Glu Leu  
 670 675 680  
 Phe Phe Met Ile Asn Thr Ser Ile Leu Leu Ile Phe Ile Phe Ile Val  
 685 690 695  
 Leu Leu Ile His Phe Glu Gly Trp Arg Ile Ser Phe Tyr Trp Asn Val  
 700 705 710 715  
 Ser Val His Arg Val Leu Gly Phe Lys Glu Ile Asp Arg Gln Thr Glu  
 720 725 730  
 Gln Phe Glu Tyr Ala Ala Tyr Ile Ile His Ala Tyr Lys Asp Lys Asp  
 735 740 745  
 Trp Val Trp Glu His Phe Ser Ser Met Glu Lys Glu Asp Gln Ser Leu  
 750 755 760  
 Lys Phe Cys Leu Glu Glu Arg Asp Phe Glu Ala Gly Val Phe Glu Leu  
 765 770 775  
 Glu Ala Ile Val Asn Ser Ile Lys Arg Ser Arg Lys Ile Ile Phe Val  
 780 785 790 795  
 Ile Thr His His Leu Leu Lys Asp Pro Leu Cys Lys Arg Phe Lys Val  
 800 805 810  
 His His Ala Val Gln Gln Ala Ile Glu Gln Asn Leu Asp Ser Ile Ile  
 815 820 825

Leu Val Phe Leu Glu Glu Ile Pro Asp Tyr Lys Leu Asn His Ala Leu  
830 835 840

Cys Leu Arg Arg Gly Met Phe Lys Ser His Cys Ile Leu Asn Trp Pro  
845 850 855

Val Gln Lys Glu Arg Ile Gly Ala Phe Arg His Lys Leu Gln Val Ala  
860 865 870 875

Leu Gly Ser Lys Asn Ser Val His  
880

<210> 7

<211> 2400

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1) .. (2397)

<400> 7

atg gag ctg aat ttc tac aaa atc ccc gac aac ctc ccc ttc tca acc 48  
Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr  
5 10 15

aag aac ctg gac ctg agc ttt aat ccc ctg agg cat tta ggc agc tat 96  
Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr  
20 25 30

agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta tcc agg tgt 144  
Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys  
35 40 45

gaa atc cag aca att gaa gat ggg gca tat cag agc cta agc cac ctc 192  
Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu  
50 55 60

tct acc tta ata ttg aca gga aac ccc atc cag agt tta gcc ctg gga 240  
Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly  
65 70 75 80

gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct gtg gag aca 288  
Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr  
85 90 95

aat cta gca tct cta gag aac ttc ccc att gga cat ctc aaa act ttg 336  
Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu

100								105					110					
aaa gaa ctt aat gtg gct cac aat ctt atc caa tct ttc aaa tta cct	384																	
Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro																		
115 120 125																		
gag tat ttt tct aat ctg acc aat cta gag cac ttg gac ctt tcc agc	432																	
Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser																		
130 135 140																		
aac aag att caa agt att tat tgc aca gac ttg cgg gtt cta cat caa	480																	
Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln																		
145 150 155 160																		
atg ccc cta ctc aat ctc tct tta gac ctg tcc ctg aac cct atg aac	528																	
Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn																		
165 170 175																		
ttt atc caa cca ggt gca ttt aaa gaa att agg ctt cat aag ctg act	576																	
Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr																		
180 185 190																		
tta aga aat aat ttt gat agt tta aat gta atg aaa act tgt att caa	624																	
Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln																		
195 200 205																		
ggg ctg gct ggt tta gaa gtc cat cgt ttg gtt ctg gga gaa ttt aga	672																	
Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg																		
210 215 220																		
aat gaa gga aac ttg gaa aag ttt gac aaa tct gct cta gag ggc ctg	720																	
Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu																		
225 230 235 240																		
tgg aat ttg acc att gaa gaa ttc cga tta gca tac tta gac tac tac	768																	
Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr																		
245 250 255																		
ctc gat gat att att gac tta ttt aat tgt ttg aca aat gtt tct tca	816																	
Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser																		
260 265 270																		
ttt tcc ctg gtg agt gtg act att gaa agg gta aaa gac ttt tct tat	864																	
Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr																		
275 280 285																		
aat ttc gga tgg caa cat tta gaa tta gtt aac tgt aaa ttt gga cag	912																	
Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln																		
290 295 300																		
ttt ccc aca ttg aaa ctc aaa tct ctc aaa agg ctt act ttc act tcc	960																	
Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser																		
305 310 315 320																		



aac	aaa	ggg	ggg	aat	gct	ttt	tca	gaa	gtt	gat	cta	cca	agc	ctt	gag	1008
Asn	Lys	Gly	Gly	Asn	Ala	Phe	Ser	Glu	Val	Asp	Leu	Pro	Ser	Leu	Glu	
				325					330						335	
ttt	cta	gat	ctc	agt	aga	aat	ggc	ttg	agt	ttc	aaa	ggg	tgc	tgt	tct	1056
Phe	Leu	Asp	Leu	Ser	Arg	Asn	Gly	Leu	Ser	Phe	Lys	Gly	Cys	Cys	Ser	
			340					345					350			
caa	agt	gat	ttt	ggg	aca	acc	agc	cta	aag	tat	tta	gat	ctg	agc	ttc	1104
Gln	Ser	Asp	Phe	Gly	Thr	Thr	Ser	Leu	Lys	Tyr	Leu	Asp	Leu	Ser	Phe	
		355					360					365				
aat	ggg	gtt	att	acc	atg	agt	tca	aac	ttc	ttg	ggc	tta	gaa	caa	cta	1152
Asn	Gly	Val	Ile	Thr	Met	Ser	Ser	Asn	Phe	Leu	Gly	Leu	Glu	Gln	Leu	
	370					375					380					
gaa	cat	ctg	gat	ttc	cag	cat	tcc	aat	ttg	aaa	caa	atg	agt	gag	ttt	1200
Glu	His	Leu	Asp	Phe	Gln	His	Ser	Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	
385					390					395					400	
tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	att	tct	cat	1248
Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	
				405					410					415		
acc	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	ttg	tcc	agt	1296
Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	
			420					425					430			
ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	aac	ttc	ctt	1344
Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	
		435					440					445				
cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	gac	ctc	tct	1392
Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	
	450					455					460					
cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	tca	ctc	tcc	1440
Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	
465					470					475					480	
agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	tca	ttg	gat	1488
Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	
			485					490						495		
acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	gat	tac	agt	1536
Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	
			500					505					510			
ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	cat	ttt	cca	1584
Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	
		515					520					525				
agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	gct	tgt	act	1632

Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr		
530						535					540						
tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	agg	cag	ctc	1680	
Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu		
545					550					555					560		
ttg	gtg	gaa	gtt	gaa	cga	atg	gaa	tgt	gca	aca	cct	tca	gat	aag	cag	1728	
Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln		
				565					570					575			
ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	aat	aag	acc	1776	
Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr		
			580					585					590				
atc	att	ggc	gtg	tcg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	gtt	gta	gca	1824	
Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser	Val	Val	Ala		
		595					600					605					
gtt	ctg	gtc	tat	aag	ttc	tat	ttt	cac	ctg	atg	ctt	ctt	gct	ggc	tgc	1872	
Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	Ala	Gly	Cys		
			610			615					620						
ata	aag	tat	ggc	aga	ggc	gaa	aac	atc	tat	gat	gcc	ttt	gtt	atc	tac	1920	
Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr		
625					630					635					640		
tea	agc	cag	gat	gag	gac	tgg	gta	agg	aat	gag	cta	gta	aag	aat	tta	1968	
Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu		
				645					650					655			
gaa	gaa	ggg	gtg	cct	cca	ttt	cag	ctc	tgc	ctt	cac	tac	aga	gac	ttt	2016	
Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe		
			660					665					670				
att	ccc	ggc	gtg	gcc	att	gct	gcc	aac	atc	atc	cat	gaa	ggc	ttc	cat	2064	
Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	Gly	Phe	His		
		675					680					685					
aaa	agc	cga	aag	gtg	att	gtt	gtg	gtg	tcc	cag	cac	ttc	atc	cag	agc	2112	
Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	Ile	Gln	Ser		
						695					700						
cgc	tgg	tgt	atc	ttt	gaa	tat	gag	att	gct	cag	acc	tgg	cag	ttt	ctg	2160	
Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu		
705					710					715					720		
agc	agt	cgt	gct	ggc	atc	atc	ttc	att	gtc	ctg	cag	aag	gtg	gag	aag	2208	
Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	Val	Glu	Lys		
				725					730					735			
acc	ctg	ctc	agg	cag	cag	gtg	gag	ctg	tac	cgc	ctt	ctc	agc	agg	aac	2256	
Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	Ser	Arg	Asn		

740

745

750

act tac ctg gag tgg gag gac agt gtc ctg ggg cgg cac atc ttc tgg 2304  
 Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp  
 755 760 765

aga cga ctc aga aaa gcc ctg ctg gat ggt aaa tca tgg aat cca gaa 2352  
 Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu  
 770 775 780

gga aca gtg ggt aca gga tgc aat tgg cag gaa gca aca tct atc tga 2400  
 Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile  
 785 790 795

<210> 8  
 <211> 799  
 <212> PRT  
 <213> Unknown

<400> 8  
 Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr  
 5 10 15

Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr  
 20 25 30

Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys  
 35 40 45

Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu  
 50 55 60

Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly  
 65 70 75 80

Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr  
 85 90 95

Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu  
 100 105 110

Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro  
 115 120 125

Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser  
 130 135 140

Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln  
 145 150 155 160

Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn  
 165 170 175

Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr  
180 185 190  
Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln  
195 200 205  
Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg  
210 215 220  
Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu  
225 230 235 240  
Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr  
245 250 255  
Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser  
260 265 270  
Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr  
275 280 285  
Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln  
290 295 300  
Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser  
305 310 315 320  
Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu  
325 330 335  
Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser  
340 345 350  
Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe  
355 360 365  
Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu  
370 375 380  
Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe  
385 390 395 400  
Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His  
405 410 415  
Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser  
420 425 430  
Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu  
435 440 445  
Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser  
450 455 460

Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser  
 465 470 475 480  
 Ser Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp  
 485 490 495  
 Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser  
 500 505 510  
 Leu Asn His Ile Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro  
 515 520 525  
 Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr  
 530 535 540  
 Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu  
 545 550 555 560  
 Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln  
 565 570 575  
 Gly Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr  
 580 585 590  
 Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala  
 595 600 605  
 Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys  
 610 615 620  
 Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr  
 625 630 635 640  
 Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu  
 645 650 655  
 Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe  
 660 665 670  
 Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His  
 675 680 685  
 Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser  
 690 695 700  
 Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu  
 705 710 715 720  
 Ser Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys  
 725 730 735  
 Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn  
 740 745 750

Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp  
755 760 765

Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu  
770 775 780

Gly Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile  
785 790 795

<210> 9  
<211> 1275  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (1) .. (1095)

<220> 9  
tgt tgg gat gtt ttt gag gga ctt tct cat ctt caa gtt ctg tat ttg 48  
Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu  
1 5 10 15  
aat cat aac tat ctt aat tcc ctt cca cca gga gta ttt agc cat ctg 96  
Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu  
20 25 30  
act gca tta agg gga cta agc ctc aac tcc aac agg ctg aca gtt ctt 144  
Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu  
35 40 45  
tct cac aat gat tta cct gct aat tta gag atc ctg gac ata tcc agg 192  
Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg  
50 55 60  
aac cag ctc cta gct cct aat cct gat gta ttt gta tca ctt agt gtc 240  
Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val  
65 70 75 80  
ttg gat ata act cat aac aag ttc att tgt gaa tgt gaa ctt agc act 288  
Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr  
85 90 95  
ttt atc aat tgg ctt aat cac acc aat gtc act ata gct ggg cct cct 336  
Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro  
100 105 110

gca	gac	ata	tat	tgt	gtg	tac	cct	gac	tcg	ttc	tct	ggg	gtt	tcc	ctc	384
Ala	Asp	Ile	Tyr	Cys	Val	Tyr	Pro	Asp	Ser	Phe	Ser	Gly	Val	Ser	Leu	
		115					120					125				
ttc	tct	ctt	tcc	acg	gaa	ggg	tgt	gat	gaa	gag	gaa	gtc	tta	aag	tcc	432
Phe	Ser	Leu	Ser	Thr	Glu	Gly	Cys	Asp	Glu	Glu	Glu	Val	Leu	Lys	Ser	
	130					135					140					
cta	aag	ttc	tcc	ctt	ttc	att	gta	tgc	act	gtc	act	ctg	act	ctg	ttc	480
Leu	Lys	Phe	Ser	Leu	Phe	Ile	Val	Cys	Thr	Val	Thr	Leu	Thr	Leu	Phe	
145					150					155					160	
ctc	atg	acc	atc	ctc	aca	gtc	aca	aag	ttc	cgg	ggc	ttc	tgt	ttt	atc	528
Leu	Met	Thr	Ile	Leu	Thr	Val	Thr	Lys	Phe	Arg	Gly	Phe	Cys	Phe	Ile	
				165					170					175		
tgt	tat	aag	aca	gcc	cag	aga	ctg	gtg	ttc	aag	gac	cat	ccc	cag	ggc	576
Cys	Tyr	Lys	Thr	Ala	Gln	Arg	Leu	Val	Phe	Lys	Asp	His	Pro	Gln	Gly	
			180					185					190			
aca	gaa	cct	gat	atg	tac	aaa	tat	gat	gcc	tat	ttg	tgc	ttc	agc	agc	624
Thr	Glu	Pro	Asp	Met	Tyr	Lys	Tyr	Asp	Ala	Tyr	Leu	Cys	Phe	Ser	Ser	
		195					200					205				
aaa	gac	ttc	aca	tgg	gtg	cag	aat	gct	ttg	ctc	aaa	cac	ctg	gac	act	672
Lys	Asp	Phe	Thr	Trp	Val	Gln	Asn	Ala	Leu	Leu	Lys	His	Leu	Asp	Thr	
	210					215					220					
caa	tac	agt	gac	caa	aac	aga	ttc	aac	ctg	tgc	ttt	gaa	gaa	aga	gac	720
Gln	Tyr	Ser	Asp	Gln	Asn	Arg	Phe	Asn	Leu	Cys	Phe	Glu	Glu	Arg	Asp	
225					230					235					240	
ttt	gtc	cca	gga	gaa	aac	cgc	att	gcc	aat	atc	cag	gat	gcc	atc	tgg	768
Phe	Val	Pro	Gly	Glu	Asn	Arg	Ile	Ala	Asn	Ile	Gln	Asp	Ala	Ile	Trp	
				245					250					255		
aac	agt	aga	aag	atc	gtt	tgt	ctt	gtg	agc	aga	cac	ttc	ctt	aga	gat	816
Asn	Ser	Arg	Lys	Ile	Val	Cys	Leu	Val	Ser	Arg	His	Phe	Leu	Arg	Asp	
			260					265					270			
ggc	tgg	tgc	ctt	gaa	gcc	ttc	agt	tat	gcc	cag	ggc	agg	tgc	tta	tct	864
Gly	Trp	Cys	Leu	Glu	Ala	Phe	Ser	Tyr	Ala	Gln	Gly	Arg	Cys	Leu	Ser	
		275					280					285				
gac	ctt	aac	agt	gct	ctc	atc	atg	gtg	gtg	gtt	ggg	tcc	ttg	tcc	cag	912
Asp	Leu	Asn	Ser	Ala	Leu	Ile	Met	Val	Val	Val	Gly	Ser	Leu	Ser	Gln	
		290				295					300					
tac	cag	ttg	atg	aaa	cat	caa	tcc	atc	aga	ggc	ttt	gta	cag	aaa	cag	960
Tyr	Gln	Leu	Met	Lys	His	Gln	Ser	Ile	Arg	Gly	Phe	Val	Gln	Lys	Gln	
305					310					315					320	
cag	tat	ttg	agg	tgg	cct	gag	gat	ctc	cag	gat	gtt	ggc	tgg	ttt	ctt	1008
Gln	Tyr	Leu	Arg	Trp	Pro	Glu	Asp	Leu	Gln	Asp	Val	Gly	Trp	Phe	Leu	

325

330

335

cat aaa ctc tct caa cag ata cta aag aaa gaa aag gaa aag aag aaa. 1056  
 His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys  
 340 345 350

gac aat aac att ccg ttg caa act gta gca acc atc tcc taatcaaagg 1105  
 Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser  
 355 360 365

agcaatttcc aacttatctc aagccacaaa taactcttca ctttgtattt gcaccaagtt 1165

atcattttgg ggtcctctct ggagggtttt ttttctttt tgctactatg aaaacaacat 1225

aaatctctca attttcgtat caaaaaaaaa aaaaaaaaaa tggcggccgc 1275

&lt;210&gt; 10

&lt;211&gt; 365

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 10

Cys Trp Asp Val Phe Glu Gly Leu Ser His Leu Gln Val Leu Tyr Leu  
 5 10 15

Asn His Asn Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu  
 20 25 30

Thr Ala Leu Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu  
 35 40 45

Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg  
 50 55 60

Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val  
 65 70 75 80

Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr  
 85 90 95

Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro  
 100 105 110

Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu  
 115 120 125

Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser  
 130 135 140

Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe  
 145 150 155 160



Leu Met Thr Ile Leu Thr Val Thr Lys Phe Arg Gly Phe Cys Phe Ile  
 165 170 175  
 Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly  
 180 185 190  
 Thr Glu Pro Asp Met Tyr Lys Tyr Asp Ala Tyr Leu Cys Phe Ser Ser  
 195 200 205  
 Lys Asp Phe Thr Trp Val Gln Asn Ala Leu Leu Lys His Leu Asp Thr  
 210 215 220  
 Gln Tyr Ser Asp Gln Asn Arg Phe Asn Leu Cys Phe Glu Glu Arg Asp  
 225 230 235 240  
 Phe Val Pro Gly Glu Asn Arg Ile Ala Asn Ile Gln Asp Ala Ile Trp  
 245 250 255  
 Asn Ser Arg Lys Ile Val Cys Leu Val Ser Arg His Phe Leu Arg Asp  
 260 265 270  
 Gly Trp Cys Leu Glu Ala Phe Ser Tyr Ala Gln Gly Arg Cys Leu Ser  
 275 280 285  
 Asp Leu Asn Ser Ala Leu Ile Met Val Val Val Gly Ser Leu Ser Gln  
 290 295 300  
 Tyr Gln Leu Met Lys His Gln Ser Ile Arg Gly Phe Val Gln Lys Gln  
 305 310 315 320  
 Gln Tyr Leu Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu  
 325 330 335  
 His Lys Leu Ser Gln Gln Ile Leu Lys Lys Glu Lys Glu Lys Lys Lys  
 340 345 350  
 Asp Asn Asn Ile Pro Leu Gln Thr Val Ala Thr Ile Ser  
 355 360 365

<210> 11  
 <211> 3138  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: primate; surmised  
 Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(3135)

<220>

<221> mat\_peptide  
 <222> (67)..(3135)

<400> 11  
 atg tgg aca ctg aag aga cta att ctt atc ctt ttt aac ata atc cta 48  
 Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu  
 -20 -15 -10

att tcc aaa ctc ctt ggg gct aga tgg ttt cct aaa act ctg ccc tgt 96  
 Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys  
 -5 -1 1 5 10

gat gtc act ctg gat gtt cca aag aac cat gtg atc gtg gac tgc aca 144  
 Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr  
 15 20 25

gac aag cat ttg aca gaa att cct gga ggt att ccc acg aac acc acg 192  
 Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr  
 30 35 40

aac ctc acc ctc acc att aac cac ata cca gac atc tcc cca gcg tcc 240  
 Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser  
 45 50 55

ttt cac aga ctg gac cat ctg gta gag atc gat ttc aga tgc aac tgt 288  
 Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys  
 60 65 70

gta cct att cca ctg ggg tca aaa aac aac atg tgc atc aag agg ctg 336  
 Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu  
 75 80 85 90

cag att aaa ccc aga agc ttt agt gga ctc act tat tta aaa tcc ctt 384  
 Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu  
 95 100 105

tac ctg gat gga aac cag cta cta gag ata ccg cag ggc ctc ccg cct 432  
 Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro  
 110 115 120

agc tta cag ctt ctc agc ctt gag gcc aac aac atc ttt tcc atc aga 480  
 Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg  
 125 130 135

aaa gag aat cta aca gaa ctg gcc aac ata gaa ata ctc tac ctg ggc 528  
 Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
 140 145 150

caa aac tgt tat tat cga aat cct tgt tat gtt tca tat tca ata gag 576  
 Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu  
 155 160 165 170

aaa gat gcc ttc cta aac ttg aca aag tta aaa gtg ctc tcc ctg aaa 624

Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser	Leu	Lys	
				175					180					185		
gat	aac	aat	gtc	aca	gcc	gtc	cct	act	gtt	ttg	cca	tct	act	tta	aca	672
Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser	Thr	Leu	Thr	
			190					195					200			
gaa	cta	tat	ctc	tac	aac	aac	atg	att	gca	aaa	atc	caa	gaa	gat	gat	720
Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile	Gln	Glu	Asp	Asp	
		205					210					215				
ttt	aat	aac	ctc	aac	caa	tta	caa	att	ctt	gac	cta	agt	gga	aat	tgc	768
Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp	Leu	Ser	Gly	Asn	Cys	
	220					225					230					
cct	cgt	tgt	tat	aat	gcc	cca	ttt	cct	tgt	gcg	ccg	tgt	aaa	aat	aat	816
Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn	
235					240					245					250	
tct	ccc	cta	cag	atc	cct	gta	aat	gct	ttt	gat	gcg	ctg	aca	gaa	tta	864
Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu	
				255					260					265		
aaa	gtt	tta	cgt	cta	cac	agt	aac	tct	ctt	cag	cat	gtg	ccc	cca	aga	912
Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg	
			270					275					280			
tgg	ttt	aag	aac	atc	aac	aaa	ctc	cag	gaa	ctg	gat	ctg	tcc	caa	aac	960
Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn	
		285					290					295				
ttc	ttg	gcc	aaa	gaa	att	ggg	gat	gct	aaa	ttt	ctg	cat	ttt	ctc	ccc	1008
Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro	
	300					305					310					
agc	ctc	atc	caa	ttg	gat	ctg	tct	ttc	aat	ttt	gaa	ctt	cag	gtc	tat	1056
Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr	
315					320					325					330	
cgt	gca	tct	atg	aat	cta	tca	caa	gca	ttt	tct	tca	ctg	aaa	agc	ctg	1104
Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu	
				335					340					345		
aaa	att	ctg	cgg	atc	aga	gga	tat	gtc	ttt	aaa	gag	ttg	aaa	agc	ttt	1152
Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe	
			350					355					360			
aac	ctc	tcg	cca	tta	cat	aat	ctt	caa	aat	ctt	gaa	gtt	ctt	gat	ctt	1200
Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu	
			365				370					375				
ggc	act	aac	ttt	ata	aaa	att	gct	aac	ctc	agc	atg	ttt	aaa	caa	ttt	1248
Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe	
	380					385					390					

aaa aga ctg aaa gtc ata gat ctt tca gtg aat aaa ata tca cct tca	1296
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro Ser	
395 400 405 410	
gga gat tca agt gaa gtt ggc ttc tgc tca aat gcc aga act tct gta	1344
Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr Ser Val	
415 420 425	
gaa agt tat gaa ccc cag gtc ctg gaa caa tta cat tat ttc aga tat	1392
Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr Phe Arg Tyr	
430 435 440	
gat aag tat gca agg agt tgc aga ttc aaa aac aaa gag gct tct ttc	1440
Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys Glu Ala Ser Phe	
445 450 455	
atg tct gtt aat gaa agc tgc tac aag tat ggg cag acc ttg gat cta	1488
Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln Thr Leu Asp Leu	
460 465 470	
agt aaa aat agt ata ttt ttt gtc aag tcc tct gat ttt cag cat ctt	1536
Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp Phe Gln His Leu	
475 480 485 490	
tet ttc ctc aaa tgc ctg aat ctg tca gga aat ctc att agc caa act	1584
Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu Ile Ser Gln Thr	
495 500 505	
ctt aat ggc agt gaa ttc caa cct tta gca gag ctg aga tat ttg gac	1632
Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp	
510 515 520	
ttc tcc aac aac cgg ctt gat tta ctc cat tca aca gca ttt gaa gag	1680
Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu	
525 530 535	
ctt cac aaa ctg gaa gtt ctg gat ata agc agt aat agc cat tat ttt	1728
Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe	
540 545 550	
caa tca gaa gga att act cat atg cta aac ttt acc aag aac cta aag	1776
Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys	
555 560 565 570	
gtt ctg cag aaa ctg atg atg aac gac aat gac atc tct tcc tcc acc	1824
Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr	
575 580 585	
agc agg acc atg gag agt gag tct ctt aga act ctg gaa ttc aga gga	1872
Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly	
590 595 600	

aat	cac	tta	gat	gtt	tta	tgg	aga	gaa	ggt	gat	aac	aga	tac	tta	caa	1920
Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn	Arg	Tyr	Leu	Gln	
		605					610					615				
tta	ttc	aag	aat	ctg	cta	aaa	tta	gag	gaa	tta	gac	atc	tct	aaa	aat	1968
Leu	Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp	Ile	Ser	Lys	Asn	
	620					625					630					
tcc	cta	agt	ttc	ttg	cct	tct	gga	gtt	ttt	gat	ggt	atg	cct	cca	aat	2016
Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly	Met	Pro	Pro	Asn	
					640					645					650	
cta	aag	aat	ctc	tct	ttg	gcc	aaa	aat	ggg	ctc	aaa	tct	ttc	agt	tgg	2064
Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys	Ser	Phe	Ser	Trp	
				655					660					665		
aag	aaa	ctc	cag	tgt	cta	aag	aac	ctg	gaa	act	ttg	gac	ctc	agc	cac	2112
Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu	Asp	Leu	Ser	His	
			670					675					680			
aac	caa	ctg	acc	act	gtc	cct	gag	aga	tta	tcc	aac	tgt	tcc	aga	agc	2160
Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn	Cys	Ser	Arg	Ser	
		685					690					695				
ctc	aag	aat	ctg	att	ctt	aag	aat	aat	caa	atc	agg	agt	ctg	acg	aag	2208
Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg	Ser	Leu	Thr	Lys	
	700					705					710					
tat	ttt	cta	caa	gat	gcc	ttc	cag	ttg	cga	tat	ctg	gat	ctc	agc	tca	2256
Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Ser	
					720					725					730	
aat	aaa	atc	cag	atg	atc	caa	aag	acc	agc	ttc	cca	gaa	aat	gtc	ctc	2304
Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro	Glu	Asn	Val	Leu	
				735					740					745		
aac	aat	ctg	aag	atg	ttg	ctt	ttg	cat	cat	aat	cgg	ttt	ctg	tgc	acc	2352
Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg	Phe	Leu	Cys	Thr	
			750					755					760			
tgt	gat	gct	gtg	tgg	ttt	gtc	tgg	tgg	gtt	aac	cat	acg	gag	gtg	act	2400
Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His	Thr	Glu	Val	Thr	
		765					770					775				
att	cct	tac	ctg	gcc	aca	gat	gtg	act	tgt	gtg	ggg	cca	gga	gca	cac	2448
Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly	Pro	Gly	Ala	His	
		780				785					790					
aag	ggc	caa	agt	gtg	atc	tcc	ctg	gat	ctg	tac	acc	tgt	gag	tta	gat	2496
Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr	Cys	Glu	Leu	Asp	
	795				800					805					810	
ctg	act	aac	ctg	att	ctg	ttc	tca	ctt	tcc	ata	tct	gta	tct	ctc	ttt	2544
Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser	Val	Ser	Leu	Phe	

815

820

825

ctc atg gtg atg atg aca gca agt cac ctc tat ttc tgg gat gtg tgg 2592  
 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp  
                     830                    835                    840

tat att tac cat ttc tgt aag gcc aag ata aag ggg tat cag cgt cta 2640  
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu  
                     845                    850                    855

ata tca cca gac tgt tgc tat gat gct ttt att gtg tat gac act aaa 2688  
 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
                     860                    865                    870

gac cca gct gtg acc gag tgg gtt ttg gct gag ctg gtg gcc aaa ctg 2736  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu  
                     875                    880                    885                    890

gaa gac cca aga gag aaa cat ttt aat tta tgt ctc gag gaa agg gac 2784  
 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp  
                     895                    900                    905

tgg tta cca ggg cag cca gtt ctg gaa aac ctt tcc cag agc ata cag 2832  
 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln  
                     910                    915                    920

ctc agc aaa aag aca gtg ttt gtg atg aca gac aag tat gca aag act 2880  
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr  
                     925                    930                    935

gaa aat ttt aag ata gca ttt tac ttg tcc cat cag agg ctc atg gat 2928  
 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp  
                     940                    945                    950

gaa aaa gtt gat gtg att atc ttg ata ttt ctt gag aag ccc ttt cag 2976  
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln  
                     955                    960                    965                    970

aag tcc aag ttc ctc cag ctc cgg aaa agg ctc tgt ggg agt tct gtc 3024  
 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val  
                     975                    980                    985

ctt gag tgg cca aca aac ccg caa gct cac cca tac ttc tgg cag tgt 3072  
 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys  
                     990                    995                    1000

cta aag aac gcc ctg gcc aca gac aat cat gtg gcc tat agt cag gtg 3120  
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val  
                     1005                    1010                    1015

ttc aag gaa acg gtc tag 3138  
 Phe Lys Glu Thr Val  
                     1020

<210> 12  
<211> 1045  
<212> PRT  
<213> Unknown

<400> 12  
Met Trp Thr Leu Lys Arg Leu Ile Leu Ile Leu Phe Asn Ile Ile Leu  
-20 -15 -10  
Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys Thr Leu Pro Cys  
-5 -1 1 5 10  
Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile Val Asp Cys Thr  
15 20 25  
Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro Thr Asn Thr Thr  
30 35 40  
Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile Ser Pro Ala Ser  
45 50 55  
Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe Arg Cys Asn Cys  
60 65 70  
Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu  
75 80 85 90  
Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr Leu Lys Ser Leu  
95 100 105  
Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro  
110 115 120  
Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg  
125 130 135  
Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile Leu Tyr Leu Gly  
140 145 150  
Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser Tyr Ser Ile Glu  
155 160 165 170  
Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser Leu Lys  
175 180 185  
Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser Thr Leu Thr  
190 195 200  
Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile Gln Glu Asp Asp  
205 210 215  
Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu Ser Gly Asn Cys

220					225					230					
Pro	Arg	Cys	Tyr	Asn	Ala	Pro	Phe	Pro	Cys	Ala	Pro	Cys	Lys	Asn	Asn
235					240					245					250
Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	Leu	Thr	Glu	Leu
				255					260					265	
Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	Val	Pro	Pro	Arg
			270					275					280		
Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	Leu	Ser	Gln	Asn
		285					290					295			
Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	His	Phe	Leu	Pro
	300					305					310				
Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	Leu	Gln	Val	Tyr
				320						325					330
Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	Leu	Lys	Ser	Leu
				335					340					345	
Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	Leu	Lys	Ser	Phe
			350					355					360		
Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	Val	Leu	Asp	Leu
		365					370					375			
Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	Phe	Lys	Gln	Phe
	380					385					390				
Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	Ile	Ser	Pro	Ser
	395			400						405					410
Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	Arg	Thr	Ser	Val
				415					420					425	
Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	Tyr	Phe	Arg	Tyr
			430					435					440		
Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	Glu	Ala	Ser	Phe
		445					450					455			
Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln	Thr	Leu	Asp	Leu
	460					465					470				
Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	Ser	Asp	Phe	Gln	His	Leu
	475			480					485						490
Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Ile	Ser	Gln	Thr
				495					500					505	



Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu Arg Tyr Leu Asp  
 510 515 520

Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr Ala Phe Glu Glu  
 525 530 535

Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn Ser His Tyr Phe  
 540 545 550

Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys  
 555 560 565 570

Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr  
 575 580 585

Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly  
 590 595 600

Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln  
 605 610 615

Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn  
 620 625 630

Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro Asn  
 635 640 645 650

Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe Ser Trp  
 655 660 665

Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp Leu Ser His  
 670 675 680

Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn Cys Ser Arg Ser  
 685 690 695

Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile Arg Ser Leu Thr Lys  
 700 705 710

Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg Tyr Leu Asp Leu Ser Ser  
 715 720 725 730

Asn Lys Ile Gln Met Ile Gln Lys Thr Ser Phe Pro Glu Asn Val Leu  
 735 740 745

Asn Asn Leu Lys Met Leu Leu Leu His His Asn Arg Phe Leu Cys Thr  
 750 755 760

Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His Thr Glu Val Thr  
 765 770 775

Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly Pro Gly Ala His  
 780 785 790

Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp  
 795 800 805 810  
 Leu Thr Asn Leu Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe  
 815 820 825  
 Leu Met Val Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp  
 830 835 840  
 Tyr Ile Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu  
 845 850 855  
 Ile Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys  
 860 865 870  
 Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys Leu  
 875 880 885 890  
 Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu Arg Asp  
 895 900 905  
 Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln Ser Ile Gln  
 910 915 920  
 Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys Tyr Ala Lys Thr  
 925 930 935  
 Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln Arg Leu Met Asp  
 940 945 950  
 Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu Lys Pro Phe Gln  
 955 960 965 970  
 Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys Gly Ser Ser Val  
 975 980 985  
 Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro Tyr Phe Trp Gln Cys  
 990 995 1000  
 Leu Lys Asn Ala Leu Ala Thr Asp Asn His Val Ala Tyr Ser Gln Val  
 1005 1010 1015  
 Phe Lys Glu Thr Val  
 1020

<210> 13

<211> 180

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised

Mus musculus

<220>

<221> CDS

<222> (1)..(177)

<400> 13

ctt	gga	aaa	cct	ctt	cag	aag	tct	aag	ttt	ctt	cag	ctc	agg	aag	aga	48
Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	
1				5					10					15		

ctc	tgc	agg	agc	tct	gtc	ctt	gag	tgg	cct	gca	aat	cca	cag	gct	cac	96
Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	
			20					25					30			

cca	tac	ttc	tgg	cag	tgc	ctg	aaa	aat	gcc	ctg	acc	aca	gac	aat	cat	144
Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	
		35					40					45				

gtg	gct	tat	agt	caa	atg	ttc	aag	gaa	aca	gtc	tag					180
Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
	50					55										

<210> 14

<211> 59

<212> PRT

<213> Unknown

<400> 14

Leu	Gly	Lys	Pro	Leu	Gln	Lys	Ser	Lys	Phe	Leu	Gln	Leu	Arg	Lys	Arg	
1				5					10					15		

Leu	Cys	Arg	Ser	Ser	Val	Leu	Glu	Trp	Pro	Ala	Asn	Pro	Gln	Ala	His	
			20					25					30			

Pro	Tyr	Phe	Trp	Gln	Cys	Leu	Lys	Asn	Ala	Leu	Thr	Thr	Asp	Asn	His	
		35					40					45				

Val	Ala	Tyr	Ser	Gln	Met	Phe	Lys	Glu	Thr	Val						
	50					55										

<210> 15

<211> 990

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (2) .. (988)

<400> 15

g aat tcc aga ctt ata aac ttg aaa aat ctc tat ttg gcc tgg aac tgc 49  
Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys  
1 5 10 15

tat ttt aac aaa gtt tgc gag aaa act aac ata gaa gat gga gta ttt 97  
Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe  
20 25 30

gaa acg ctg aca aat ttg gag ttg cta tca cta tct ttc aat tct ctt 145  
Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu  
35 40 45

tca cat gtg cca ccc aaa ctg cca agc tcc cta cgc aaa ctt ttt ctg 193  
Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu  
50 55 60

agc aac acc cag atc aaa tac att agt gaa gaa gat ttc aag gga ttg 241  
Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu  
65 70 75 80

atg aat tta aca tta cta gat tta agc ggg aac tgt ccg agg tgc ttc 289  
Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe  
85 90 95

aat gcc cca ttt cca tgc gtg cct tgt gat ggt ggt gct tca att aat 337  
Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn  
100 105 110

ata gat cgt ttt gct ttt caa aac ttg acc caa ctt cga tac cta aac 385  
Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn  
115 120 125

ctc tct agc act tcc ctc agg aag att aat gct gcc tgg ttt aaa aat 433  
Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn  
130 135 140

atg cct cat ctg aag gtg ctg gat ctt gaa ttc aac tat tta gtg gga 481  
Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly  
145 150 155 160

gaa ata gcc tct ggg gca ttt tta acg atg ctg ccc cgc tta gaa ata 529  
Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile  
165 170 175

ctt gac ttg tct ttt aac tat ata aag ggg agt tat cca cag cat att 577  
Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile  
180 185 190

aat att tcc aga aac ttc tct aaa ctt ttg tct cta cgg gca ttg cat 625  
Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His

195

200

205

tta aga ggt tat gtg ttc cag gaa ctc aga gaa gat gat ttc cag ccc 673  
 Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro  
 210 215 220

ctg atg cag ctt cca aac tta tcg act atc aac ttg ggt att aat ttt 721  
 Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe  
 225 230 235 240

att aag caa atc gat ttc aaa ctt ttc caa aat ttc tcc aat ctg gaa 769  
 Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu  
 245 250 255

att att tac ttg tca gaa aac aga ata tca ccg ttg gta aaa gat acc 817  
 Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr  
 260 265 270

cgg cag agt tat gca aat agt tcc tct ttt caa cgt cat atc cgg aaa 865  
 Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys  
 275 280 285

cgg cgc tca aca gat ttt gag ttt gac cca cat tcg aac ttt tat cat 913  
 Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His  
 290 295 300

ttc acc cgt cct tta ata aag cca caa tgt gct gct tat gga aaa gcc 961  
 Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala  
 305 310 315 320

tta gat tta agc ctc aac agt att ttc tt 990  
 Leu Asp Leu Ser Leu Asn Ser Ile Phe  
 325

&lt;210&gt; 16

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 16

Asn Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys  
 1 5 10 15

Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe  
 20 25 30

Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu  
 35 40 45

Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu  
 50 55 60

Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu

65	70	75	80
Ile Asn Leu Thr	Leu Leu Asp Leu Ser Gly	Asn Cys Pro Arg Cys Phe	85 90 95
Asn Ala Pro Phe	Pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn		100 105 110
Ile Asp Arg	Phe Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn		115 120 125
Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn			130 135 140
Met Pro His Leu Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly			145 150 155 160
Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile			165 170 175
Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile			180 185 190
Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His			195 200 205
Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro			210 215 220
Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe			225 230 235 240
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu			245 250 255
Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr			260 265 270
Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys			275 280 285
Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His			290 295 300
Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala			305 310 315 320
Leu Asp Leu Ser Leu Asn Ser Ile Phe			325

<210> 17  
 <211> 1557

<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (1)..(513)

<220>  
<221> misc\_feature  
<222> (93)..(149)  
<223> Xaa translation depends on genetic code

<400> 17  
cag tct ctt tcc aca tcc caa act ttc tat gat gct tac att tct tat 48  
Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr  
1 5 10 15  
gac acc aaa gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc 96  
Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg  
20 25 30  
tac cac ctt gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag 144  
Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu  
35 40 45  
gag agg gat tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag 192  
Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln  
50 55 60  
agc atc aac caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat 240  
Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr  
65 70 75 80  
gca aaa agc tgg aac ttt aaa aca gct ttt tac ttg gsc ttg cag agg 288  
Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg  
85 90 95  
cta atg ggt gag aac atg gat gtg att ata ttt atc ctg ctg gag cca 336  
Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro  
100 105 110  
gtg tta cag cat tct ccg tat ttg agg cta cgg cag cgg atc tgt aag 384  
Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys  
115 120 125  
agc tcc atc ctc cag tgg cct gac aac ccg aag gca gaa agg ttg ttt 432  
Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe  
130 135 140  
tgg caa act ctg wga aat gtg gtc ttg act gaa aat gat tca cgg tat 480

Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr  
 145 150 155 160

aac aat atg tat gtc gat tcc att aag caa tac taactgacgt taagtcatga 533  
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr  
 165 170

tttcgcgccca taataaagat gcaaaggaat gacatttcng tattagttat ctattgctan 593  
 ggtaacnaaa ttantcccaa aaancttang tnggtttnaa aacaacnaca ttntgctggn 653  
 cccacagttt ttgaggggtca ggagtcacagg cccagcataa ctgggtcttc tgcttcaggg 713  
 tgtctncaga ggctgcaatg taggtgttca ccagagacat aggcacact ggggtcacac 773  
 tncatgtggt tgttttctgg attcaattcc tcctgggcta ttggccaaag gctataactca 833  
 tgtaagccat gcgagcctat cccacaangg cagcttgctt catcagagct agcaaaaaag 893  
 agaggttgct agcaagatga agtcacaatc ttttgaatc gaatcaaaaa agtgatatct 953  
 catcactttg gccatattct atttggtaga agtaaaccac aggtcccacc agtccatgg 1013  
 ggtgaccac ctgagtcag ggaaaacagc tgaagaccaa gatggtgagc tctgattgct 1073  
 tcagttgggtc atcaactatt ttcccttgac tgctgtcctg ggatggccgg ctatcttgat 1133  
 ggatagattg tgaatatcag gaggccaggg atcactgtgg accatcttag cagttgacct 1193  
 aacacatctt cttttcaata tctaagaact tttgccactg tgactaatgg tcctaataatt 1253  
 aagctgttgt ttatatattat catatatcta tggctacatg gttatattat gctgtgggtg 1313  
 ggttcgggtt tattttacagt tgcttttaca aatatttgct gtaacatttg acttctaagg 1373  
 ttttagatgcc atttaagaac tgagatggat agctttttaa gcacttttta cttcttacca 1433  
 ttttttaaaa gtatgcagct aaattcgaag cttttggtct atattgttaa ttgccattgc 1493  
 tgtaaattctt aaaatgaatg aataaaaatg tttcatttta aaaaaaaaaa aaaaaaaaaa 1553  
 aaaa 1557

<210> 18  
 <211> 171  
 <212> PRT  
 <213> Unknown

<400> 18  
 Gln Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr  
 1 5 10 15



Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg  
                   20                  25                  30  
 Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu  
                   35                  40                  45  
 Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln  
                   50                  55                  60  
 Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr  
                   65                  70                  75                  80  
 Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe Tyr Leu Xaa Leu Gln Arg  
                   85                  90                  95  
 Leu Met Gly Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro  
                   100                  105                  110  
 Val Leu Gln His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys  
                   115                  120                  125  
 Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Arg Leu Phe  
                   130                  135                  140  
 Trp Gln Thr Leu Xaa Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr  
                   145                  150                  155                  160  
 Asn Asn Met Tyr Val Asp Ser Ile Lys Gln Tyr  
                   165                  170

<210> 19

<211> 629

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(486)

<220>

<221> misc\_feature

<222> (48)..(75)

<223> Xaa translation depends on genetic code

<400> 19

aat gaa ttg atc ccc aat cta gag aag gaa gat ggt tct atc ttg att      48  
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile  
   1                  5                  10                  15

tgc ctt tat gaa agc tac ttt gac cct ggc aaa agc att agt gaa aat	96
Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn	
20 25 30	
att gta agc ttc att gag aaa agc tat aag tcc atc ttt gtt ttg tcy	144
Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa	
35 40 45	
ccc aac ttt gtc cag aat gag tgg tgc cat tat gaa ttc tac ttt gcc	192
Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala	
50 55 60	
cac cac aat ctc ttc cat gaa aat tct gat cay ata att ctt atc tta	240
His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu	
65 70 75 80	
ctg gaa ccc att cca ttc tat tgc att ccc acc agg tat cat aaa ctg	288
Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu	
85 90 95	
gaa gct ctc ctg gaa aaa aaa gca tac ttg gaa tgg ccc aag gat agg	336
Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg	
100 105 110	
cgt aaa tgt ggg ctt ttc tgg gca aac ctt cga gct gct gtt aat gtt	384
Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val	
115 120 125	
aat gta tta gcc acc aga gaa atg tat gaa ctg cag aca ttc aca gag	432
Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu	
130 135 140	
tta aat gaa gag tct cga ggt tct aca atc tct ctg atg aga aca gac	480
Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp	
145 150 155 160	
tgt cta taaaatccca cagtccttgg gaagttgggg accacataca ctgttgggat	536
Cys Leu	
gtacattgat acaaccttta tgatggcaat ttgacaatat ttattaaaat aaaaaatggt	596
tattcccttc aaaaaaaaaa aaaaaaaaaa aaa	629

<210> 20  
 <211> 162  
 <212> PRT  
 <213> Unknown

<400> 20  
 Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp Gly Ser Ile Leu Ile  
 1 5 10 15

Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn  
                   20                                  25                                  30  
 Ile Val Ser Phe Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Xaa  
                   35                                  40                                  45  
 Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala  
                   50                                  55                                  60  
 His His Asn Leu Phe His Glu Asn Ser Asp Xaa Ile Ile Leu Ile Leu  
                   65                                  70                                  75                                  80  
 Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu  
                                   85                                  90                                  95  
 Glu Ala Leu Leu Glu Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg  
                                   100                                  105                                  110  
 Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Val Asn Val  
                   115                                  120                                  125  
 Asn Val Leu Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu  
                   130                                  135                                  140  
 Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp  
                   145                                  150                                  155                                  160  
 Cys Leu

<210> 21

<211> 427

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(426)

<400> 21

aag aac tcc aaa gaa aac ctc cag ttt cat gct ttt att tca tat agt 48  
 Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser  
   1                                  5                                  10                                  15

gaa cat gat tct gcc tgg gtg aaa agt gaa ttg gta cct tac cta gaa 96  
 Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu  
                   20                                  25                                  30

aaa gaa gat ata cag att tgt ctt cat gag aga aac ttt gtc cct ggc 144

Lys Glu Asp Ile Gln Ile Cys Leu His Glu Arg Asn Phe Val Pro Gly  
 35 40 45

aag agc att gtg gaa aat atc atc aac tgc att gag aag agt tac aag 192  
 Lys Ser Ile Val Glu Asn Ile Ile Asn Cys Ile Glu Lys Ser Tyr Lys  
 50 55 60

tcc atc ttt gtt ttg tct ccc aac ttt gtc cag agt gag tgg tgc cat 240  
 Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser Glu Trp Cys His  
 65 70 75 80

tac gaa ctc tat ttt gcc cat cac aat ctc ttt cat gaa gga tct aat 288  
 Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His Glu Gly Ser Asn  
 85 90 95

aac tta atc ctc atc tta ctg gaa ccc att cca cag aac agc att ccc 336  
 Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln Asn Ser Ile Pro  
 100 105 110

aac aag tac cac aag ctg aag gct ctc atg acg cag cgg act tat ttg 384  
 Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu  
 115 120 125

cag tgg ccc aag gag aaa agc aaa cgt ggg ctc ttt tgg gct a 427  
 Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala  
 130 135 140

<210> 22

<211> 142

<212> PRT

<213> Unknown

<400> 22

Lys Asn Ser Lys Glu Asn Leu Gln Phe His Ala Phe Ile Ser Tyr Ser  
 1 5 10 15

Glu His Asp Ser Ala Trp Val Lys Ser Glu Leu Val Pro Tyr Leu Glu  
 20 25 30

Lys Glu Asp Ile Gln Ile Cys Leu His Glu Arg Asn Phe Val Pro Gly  
 35 40 45

Lys Ser Ile Val Glu Asn Ile Ile Asn Cys Ile Glu Lys Ser Tyr Lys  
 50 55 60

Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Ser Glu Trp Cys His  
 65 70 75 80

Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His Glu Gly Ser Asn  
 85 90 95

Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Pro Gln Asn Ser Ile Pro

	100		105		110
Asn Lys Tyr His Lys Leu Lys Ala Leu Met Thr Gln Arg Thr Tyr Leu					
	115		120		125
Gln Trp Pro Lys Glu Lys Ser Lys Arg Gly Leu Phe Trp Ala					
	130		135		140

<210> 23  
 <211> 662  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(627)  
 <220>  
 <221> misc\_feature  
 <222> (18)..(136)  
 <223> Xaa translation depends on genetic code

<400> 23	
gct tcc acc tgt gcc tgg cct ggc ttc cct ggc ggg ggc ggc aaa gtg	48
Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Gly Lys Val	
	5 10 15
ggc gar atg agg atg ccc tgc cct acg atg cct tcg tgg tct tcg aca	96
Gly Xaa Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr	
	20 25 30
aaa cgc rga gcg cag tgg cag act ggg tgt aca acg agc ttc ggg ggc	144
Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly	
	35 40 45
agc tgg agg agt gcc gtg ggc gct ggg cac tcc gcc tgt gcc tgg agg	192
Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg	
	50 55 60
aac gcg act ggc tgc ctg gca aaa ccc tct ttg aga acc tgt ggg cct	240
Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro	
	65 70 75 80
cgg tct atg gca gcc gca aga cgc tgt ttg tgc tgg ccc aca cgg acc	288
Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr	
	85 90 95
ggg tca gtg gtc tct tgc gcg cca ktt ntc ctg ctg gcc cag cag cgc	336
Gly Ser Val Val Ser Cys Ala Pro Xaa Xaa Leu Leu Ala Gln Gln Arg	

100										105					110					
ctg	ctg	gar	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	atc	cta	ang	cct	384				
Leu	Leu	Xaa	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Xaa	Pro					
		115					120					125								
gac	ggc	caa	gcc	tcc	cga	cta	cnn	gat	gcg	ctg	acc	agc	gcc	tct	gcc	432				
Asp	Gly	Gln	Ala	Ser	Arg	Leu	Xaa	Asp	Ala	Leu	Thr	Ser	Ala	Ser	Ala					
	130					135					140									
gcc	aga	gtg	tcc	tcc	tct	ggc	ccc	acc	agc	cca	gtg	gtc	gcg	cag	ctt	480				
Ala	Arg	Val	Ser	Ser	Ser	Gly	Pro	Thr	Ser	Pro	Val	Val	Ala	Gln	Leu					
145					150					155					160					
ctg	agg	cca	gca	tgc	atg	gcc	ctg	acc	agg	gac	aac	cac	cac	ttc	tat	528				
Leu	Arg	Pro	Ala	Cys	Met	Ala	Leu	Thr	Arg	Asp	Asn	His	His	Phe	Tyr					
				165					170					175						
aac	cgg	aac	ttc	tgc	cag	gga	acc	cac	ggc	cga	ata	gcc	gtg	agc	cgg	576				
Asn	Arg	Asn	Phe	Cys	Gln	Gly	Thr	His	Gly	Arg	Ile	Ala	Val	Ser	Arg					
			180					185					190							
aat	cct	gca	cgg	tgc	cac	ctc	cac	aca	cac	cta	aca	tat	gcc	tgc	ctg	624				
Asn	Pro	Ala	Arg	Cys	His	Leu	His	Thr	His	Leu	Thr	Tyr	Ala	Cys	Leu					
		195				200						205								
atc	tgaccaacac	atgctcgcca	ccctcaccac	acacc												662				
Ile																				

<210> 24  
 <211> 209  
 <212> PRT  
 <213> Unknown

<400> 24  
 Ala Ser Thr Cys Ala Trp Pro Gly Phe Pro Gly Gly Gly Gly Lys Val  
 1 5 10 15  
 Gly Xaa Met Arg Met Pro Cys Pro Thr Met Pro Ser Trp Ser Ser Thr  
 20 25 30  
 Lys Arg Xaa Ala Gln Trp Gln Thr Gly Cys Thr Thr Ser Phe Gly Gly  
 35 40 45  
 Ser Trp Arg Ser Ala Val Gly Ala Gly His Ser Ala Cys Ala Trp Arg  
 50 55 60  
 Asn Ala Thr Gly Cys Leu Ala Lys Pro Ser Leu Arg Thr Cys Gly Pro  
 65 70 75 80  
 Arg Ser Met Ala Ala Ala Arg Arg Cys Leu Cys Trp Pro Thr Arg Thr  
 85 90 95



tcg cgc ctg gct ggg act ctg atc cca gcc atg gcc ttc ctc tcc tgc	163
Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe Leu Ser Cys	
-15 -10 -5	
gtg aga cca gaa agc tgg gag ccc tgc gtg gag gtt cct aat att act	211
Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val Pro Asn Ile Thr	
-1 1 5 10	
tat caa tgc atg gag ctg aat ttc tac aaa atc ccc gac aac ctc ccc	259
Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro	
15 20 25	
ttc tca acc aag aac ctg gac ctg agc ttt aat ccc ctg agg cat tta	307
Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu	
30 35 40 45	
ggc agc tat agc ttc ttc agt ttc cca gaa ctg cag gtg ctg gat tta	355
Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu	
50 55 60	
tcc agg tgt gaa atc cag aca att gaa gat ggg gca tat cag agc cta	403
Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu	
65 70 75	
agg cac ctc tct acc tta ata ttg aca gga aac ccc atc cag agt tta	451
Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu	
80 85 90	
ggc ctg gga gcc ttt tct gga cta tca agt tta cag aag ctg gtg gct	499
Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala	
95 100 105	
gtg gag aca aat cta gca tct cta gag aac ttc ccc att gga cat ctc	547
Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu	
110 115 120 125	
aaa act ttg aaa gaa ctt aat gtg gct cac aat ctt atc caa tct ttc	595
Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe	
130 135 140	
aaa tta cct gag tat ttt tct aat ctg acc aat cta gag cac ttg gac	643
Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp	
145 150 155	
ctt tcc agc aac aag att caa agt att tat tgc aca gac ttg cgg gtt	691
Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val	
160 165 170	
cta cat caa atg ccc cta ctc aat ctc tct tta gac ctg tcc ctg aay	739
Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Xaa	
175 180 185	



cct atg aac ttt atc caa cca ggt gca ttt aaa gaa att agg ctt cat	787
Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His	
190 195 200 205	
aag ctg act tta aga aat aat ttt gat agt tta aat gta atg aaa act	835
Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr	
210 215 220	
tgt att caa ggt ctg gct ggt tta gaa gtc cat cgt ttg gtt ctg gga	883
Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly	
225 230 235	
gaa ttt aga aat gaa gga aac ttg gaa aag ttt gac aaa tct gct cta	931
Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu	
240 245 250	
gag ggc ctg tgc aat ttg acc att gaa gaa ttc cga tta gca tac tta	979
Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu	
255 260 265	
gac tac tac ctc gat gat att att gac tta ttt aat tgt ttg aca aat	1027
Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn	
270 275 280 285	
gtt tct tca ttt tcc ctg gtg agt gtg act att gaa agg gta aaa gac	1075
Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp	
290 295 300	
ttt tct tat aat ttc gga tgg caa cat tta gaa tta gtt aac tgt aaa	1123
Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys	
305 310 315	
ttt gga cag ttt ccc aca ttg aaa ctc aaa tct ctc aaa agg ctt act	1171
Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr	
320 325 330	
ttc act tcc aac aaa ggt ggg aat gct ttt tca gaa gtt gat cta cca	1219
Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro	
335 340 345	
agc ctt gag ttt cta gat ctc agt aga aat ggc ttg agt ttc aaa ggt	1267
Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly	
350 355 360 365	
tgc tgt tct caa agt gat ttt ggg aca acc agc cta aag tat tta gat	1315
Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp	
370 375 380	
ctg agc ttc aat ggt gtt att acc atg agt tca aac ttc ttg ggc tta	1363
Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu	
385 390 395	
gaa caa cta gaa cat ctg gat ttc cag cat tcc aat ttg aaa caa atg	1411
Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met	

400										405					410					
agt	gag	ttt	tca	gta	ttc	cta	tca	ctc	aga	aac	ctc	att	tac	ctt	gac	1459				
Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	Leu	Ile	Tyr	Leu	Asp					
415						420					425									
att	tct	cat	act	cac	acc	aga	gtt	gct	ttc	aat	ggc	atc	ttc	aat	ggc	1507				
Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	Gly	Ile	Phe	Asn	Gly					
430						435					440				445					
ttg	tcc	agt	ctc	gaa	gtc	ttg	aaa	atg	gct	ggc	aat	tct	ttc	cag	gaa	1555				
Leu	Ser	Ser	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	Asn	Ser	Phe	Gln	Glu					
450						455					460									
aac	ttc	ctt	cca	gat	atc	ttc	aca	gag	ctg	aga	aac	ttg	acc	ttc	ctg	1603				
Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	Asn	Leu	Thr	Phe	Leu					
465						470					475									
gac	ctc	tct	cag	tgt	caa	ctg	gag	cag	ttg	tct	cca	aca	gca	ttt	aac	1651				
Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	Pro	Thr	Ala	Phe	Asn					
480						485					490									
tca	ctc	tcc	agt	ctt	cag	gta	cta	aat	atg	agc	cac	aac	aac	ttc	ttt	1699				
Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	His	Asn	Asn	Phe	Phe					
495						500					505									
tca	ttg	gat	acg	ttt	cct	tat	aag	tgt	ctg	aac	tcc	ctc	cag	gtt	ctt	1747				
Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	Ser	Leu	Gln	Val	Leu					
510						515					520				525					
gat	tac	agt	ctc	aat	cac	ata	atg	act	tcc	aaa	aaa	cag	gaa	cta	cag	1795				
Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	Lys	Gln	Glu	Leu	Gln					
530						535					540									
cat	ttt	cca	agt	agt	cta	gct	ttc	tta	aat	ctt	act	cag	aat	gac	ttt	1843				
His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	Thr	Gln	Asn	Asp	Phe					
545						550					555									
gct	tgt	act	tgt	gaa	cac	cag	agt	ttc	ctg	caa	tgg	atc	aag	gac	cag	1891				
Ala	Cys	Thr	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	Trp	Ile	Lys	Asp	Gln					
560						565					570									
agg	cag	ctc	ttg	gtg	gaa	gtt	gaa	cga	atg	gaa	tgt	gca	aca	cct	tca	1939				
Arg	Gln	Leu	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	Cys	Ala	Thr	Pro	Ser					
575						580					585									
gat	aag	cag	ggc	atg	cct	gtg	ctg	agt	ttg	aat	atc	acc	tgt	cag	atg	1987				
Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	Ile	Thr	Cys	Gln	Met					
590						595					600				605					
aat	aag	acc	atc	att	ggg	gtg	tgg	gtc	ctc	agt	gtg	ctt	gta	gta	tct	2035				
Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	Val	Leu	Val	Val	Ser					
610						615					620									

gtt	gta	gca	gtt	ctg	gtc	tat	aag	ttc	tat	ttt	cac	ctg	atg	ctt	ctt	2083
Val	Val	Ala	Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	His	Leu	Met	Leu	Leu	
			625					630					635			
gct	ggc	tgc	ata	aag	tat	ggt	aga	ggt	gaa	aac	atc	tat	gat	gcc	ttt	2131
Ala	Gly	Cys	Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	Ile	Tyr	Asp	Ala	Phe	
		640					645					650				
gtt	atc	tac	tca	agc	cag	gat	gag	gac	tgg	gta	agg	aat	gag	cta	gta	2179
Val	Ile	Tyr	Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	Arg	Asn	Glu	Leu	Val	
	655					660					665					
aag	aat	tta	gaa	gaa	ggg	gtg	cct	cca	ttt	cag	ctc	tgc	ctt	cac	tac	2227
Lys	Asn	Leu	Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	Leu	Cys	Leu	His	Tyr	
670					675					680					685	
aga	gac	ttt	att	ccc	ggt	gtg	gcc	att	gct	gcc	aac	atc	atc	cat	gaa	2275
Arg	Asp	Phe	Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	Asn	Ile	Ile	His	Glu	
				690					695					700		
ggg	ttc	cat	aaa	agc	cga	aag	gtg	att	ggt	gtg	gtg	tcc	cag	cac	ttc	2323
Gly	Phe	His	Lys	Ser	Arg	Lys	Val	Ile	Val	Val	Val	Ser	Gln	His	Phe	
			705					710					715			
atc	cag	agc	cgc	tgg	tgt	atc	ttt	gaa	tat	gag	att	gct	cag	acc	tgg	2371
Ile	Gln	Ser	Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	Ile	Ala	Gln	Thr	Trp	
		720					725					730				
cag	ttt	ctg	agc	agt	cgt	gct	ggt	atc	atc	ttc	att	gtc	ctg	cag	aag	2419
Gln	Phe	Leu	Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	Ile	Val	Leu	Gln	Lys	
	735					740					745					
gtg	gag	aag	acc	ctg	ctc	agg	cag	cag	gtg	gag	ctg	tac	cgc	ctt	ctc	2467
Val	Glu	Lys	Thr	Leu	Leu	Arg	Gln	Gln	Val	Glu	Leu	Tyr	Arg	Leu	Leu	
750					755					760					765	
agc	agg	aac	act	tac	ctg	gag	tgg	gag	gac	agt	gtc	ctg	ggg	cgg	cac	2515
Ser	Arg	Asn	Thr	Tyr	Leu	Glu	Trp	Glu	Asp	Ser	Val	Leu	Gly	Arg	His	
				770					775					780		
atc	ttc	tgg	aga	cga	ctc	aga	aaa	gcc	ctg	ctg	gat	ggt	aaa	tca	tgg	2563
Ile	Phe	Trp	Arg	Arg	Leu	Arg	Lys	Ala	Leu	Leu	Asp	Gly	Lys	Ser	Trp	
			785					790					795			
aat	cca	gaa	gga	aca	gtg	ggt	aca	gga	tgc	aat	tgg	cag	gaa	gca	aca	2611
Asn	Pro	Glu	Gly	Thr	Val	Gly	Thr	Gly	Cys	Asn	Trp	Gln	Glu	Ala	Thr	
		800					805					810				
tct	atc	tgaagaggaa	aaataaaaac	ctcctgaggc	atttcttgcc	cagctggggtc										2667
Ser	Ile															
	815															

tgagtaattc catggtgcac tagatatgca gggctgctaa tctcaaggag cttccagtgc 2787  
agagggaata aatgctagac taaaatacag agtcttccag gtgggcattt caaccaactc 2847  
agtcaaggaa cccatgacaa agaaagtcac ttcaactctt acctcatcaa gttgaataaa 2907  
gacagagaaa acagaaagag acattgttct tttcctgagt cttttgaatg gaaattgtat 2967  
tatgttatag ccatcataaa accatttttg tagttttgac tgaactgggt gttcactttt 3027  
tcctttttga ttgaatacaa tttaaattct acttgatgac tgcagtcgac aaggggctcc 3087  
tgatgcaaga tgccccttcc attttaagtc tgtctcctta cagakgttaa agtctantgg 3147  
ctaattccta aggaaacctg attaacacat gtcacaacc atcctgggtca ttctcganac 3207  
tggtctatct ttttaactaat caccctgat atatttttat ttttatatat ccagttttca 3267  
tttttttacg tcttgccctat aagctaatat cataaataag gttgtttaag acgtgcttca 3327  
aatatccata ttaaccacta tttttcaagg aagtatggaa aagtacactc tgtcactttg 3387  
tactcgatg tcattccaaa gttattgcct actaagtaat gactgtcatg aaagcagcat 3447  
tgaataatt tgtttaaagg gggcactctt ttaaacggga agaaaatttc cgcttcctgg 3507  
tttatcatg gacaatttgg gctakaggca kgaaggaagt gggatkacct caggangtca 3567  
ccttttcttg attccagaaa catatgggct gataaaccgc gggtgacctc atgaaatgag 3627  
tgcagcaga wgtttatctt tttcagaaca agtgatgttt gatggacctm tgaatctmtt 3687  
tagggagaca cagatggctg ggatccctcc cctgtacctt tctcactgmc aggagaacta 3747  
cgtgtgaagg tattcaaggc agggagtata cattgctgtt tcctgttggg caatgctcct 3807  
tgaccacatt ttgggaagag tggatgttat cattgagaaa acaatgtgtc tggaattaat 3867  
ggggttctta taaagaaggt tcccagaaaa gaatgttcat tccagcttct tcaggaaaca 3927  
ggaacattca aggaaaagga caatcaggat gtcacaggg aatgaaaat aaaaaccaca 3987  
atgagatate accttatacc aggtagatgg ctactataaa aaaatgaagt gtcacaggg 4047  
atatagagaa attggaacct ttcttactg ctggaggga tggaaaatgg tgtagccgtt 4107  
atgaaaaaca gtacggaggt ttctcaaaaa ttaaaaatag aactgctata tgatccagca 4167  
atctcacttc tgtatatata cccaaaataa ttgaaatcag aatttcaaga aatatttac 4227  
actcccatgt tcattgtggc actcttcaca atcactgttt ccaaagttat ggaacaacc 4287

caaattttcca ttggaaaata aatggacaaa ggaaatgtgc atataacgta caatggggat 4347  
 attattcagc ctaaaaaaag gggggatcct gttatttatg acaacatgaa taaacccgga 4407  
 ggccattatg ctatgtaaaa tgagcaagta acagaaagac aaatactgcc tgatttcatt 4467  
 tatatgaggt tctaaaatag tcaaactcat agaagcagag aatagaacag tggttcctag 4527  
 ggaaaaggag gaaggagaa atgaggaaat agggagttgt ctaattggta taaaattata 4587  
 gtatgcaaga tgaattagct ctaaagatca gctgtatagc agagttcgta taatgaacaa 4647  
 tactgtatta tgcacttaac attttggttaa gagggtagct ctcattgttaa gtgttcttac 4707  
 catatacata tacacaagga agcttttgga ggtgatggat atatttatta ccttgattgt 4767  
 ggtgatgggt tgacaggtat gtgactatgt ctaaactcat caaattgtat acattaaata 4827  
 tatgcagttt tataatatca aaaaaaaaaa aaaaaaaaaa 4865

<210> 26  
 <211> 837  
 <212> PRT  
 <213> Unknown

<400> 26  
 Met Ser Ala Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala Phe  
 -20 -15 -10  
 Leu Ser Cys Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val Pro  
 -5 -1 1 5 10  
 Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp  
 15 20 25  
 Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu  
 30 35 40  
 Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu Leu Gln Val  
 45 50 55  
 Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr  
 60 65 70  
 Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile  
 75 80 85 90  
 Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys  
 95 100 105  
 Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile  
 110 115 120

Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn Leu Ile  
 125 130 135  
 Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu  
 140 145 150  
 His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp  
 155 160 165 170  
 Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu Asp Leu  
 175 180 185  
 Ser Leu Xaa Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile  
 190 195 200  
 Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu Asn Val  
 205 210 215  
 Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His Arg Leu  
 220 225 230  
 Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys  
 235 240 245 250  
 Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu  
 255 260 265  
 Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys  
 270 275 280  
 Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile Glu Arg  
 285 290 295  
 Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu Leu Val  
 300 305 310  
 Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys  
 315 320 325 330  
 Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser Glu Val  
 335 340 345  
 Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser  
 350 355 360  
 Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys  
 365 370 375  
 Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser Asn Phe  
 380 385 390  
 Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser Asn Leu  
 395 400 405 410

Lys Gln Met Ser Glu Phe Ser Val Phe Leu Ser Leu Arg Asn Leu Ile  
 415 420 425  
 Tyr Leu Asp Ile Ser His Thr His Thr Arg Val Ala Phe Asn Gly Ile  
 430 435 440  
 Phe Asn Gly Leu Ser Ser Leu Glu Val Leu Lys Met Ala Gly Asn Ser  
 445 450 455  
 Phe Gln Glu Asn Phe Leu Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu  
 460 465 470  
 Thr Phe Leu Asp Leu Ser Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr  
 475 480 485 490  
 Ala Phe Asn Ser Leu Ser Ser Leu Gln Val Leu Asn Met Ser His Asn  
 495 500 505  
 Asn Phe Phe Ser Leu Asp Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu  
 510 515 520  
 Gln Val Leu Asp Tyr Ser Leu Asn His Ile Met Thr Ser Lys Lys Gln  
 525 530 535  
 Glu Leu Gln His Phe Pro Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln  
 540 545 550  
 Asn Asp Phe Ala Cys Thr Cys Glu His Gln Ser Phe Leu Gln Trp Ile  
 555 560 565 570  
 Lys Asp Gln Arg Gln Leu Leu Val Glu Val Glu Arg Met Glu Cys Ala  
 575 580 585  
 Thr Pro Ser Asp Lys Gln Gly Met Pro Val Leu Ser Leu Asn Ile Thr  
 590 595 600  
 Cys Gln Met Asn Lys Thr Ile Ile Gly Val Ser Val Leu Ser Val Leu  
 605 610 615  
 Val Val Ser Val Val Ala Val Leu Val Tyr Lys Phe Tyr Phe His Leu  
 620 625 630  
 Met Leu Leu Ala Gly Cys Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr  
 635 640 645 650  
 Asp Ala Phe Val Ile Tyr Ser Ser Gln Asp Glu Asp Trp Val Arg Asn  
 655 660 665  
 Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Pro Phe Gln Leu Cys  
 670 675 680  
 Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile  
 685 690 695

Ile His Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser  
700 705 710

Gln His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala  
715 720 725 730

Gln Thr Trp Gln Phe Leu Ser Ser Arg Ala Gly Ile Ile Phe Ile Val  
735 740 745

Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu Leu Tyr  
750 755 760

Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser Val Leu  
765 770 775

Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu Asp Gly  
780 785 790

Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn Trp Gln  
795 800 805 810

Glu Ala Thr Ser Ile  
815

<210> 27

<211> 300

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism:rodent; surmised  
Mus musculus

<220>

<221> CDS

<222> (1)..(300)

<220>

<221> misc\_feature

<222> (62)..(100)

<223> Xaa translation depends on genetic code

<400> 27

tcc tat tct atg gaa aaa gat gct ttc cta ttt atg aga aat ttg aag 48  
Ser Tyr Ser Met Glu Lys Asp Ala Phe Leu Phe Met Arg Asn Leu Lys  
1 5 10 15

gtt ctc tca cta aaa gat aac aat gtc aca gct gtc ccc acc act ttg 96  
Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu  
20 25 30



cca cct aat tta cta gag ctc tat ctt tat aac aat atc att aag aaa	144
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
atc caa gaa aat gat ttc aat aac ctc aat gag ttg caa gtn ctt gac	192
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
cta ngf gga aat tgc cct cga tgt nat aat gtc cca tat ccg tgt aca	240
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
ccg tgt gaa aat aat tcc ccc tta cag atc cat gan aat gct ttc aat	288
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
85 90 95	
tca tcg aca gan	300
Ser Ser Thr Xaa	
100	

<210> 28  
 <211> 100  
 <212> PRT  
 <213> Unknown

<400> 28	
Ser Tyr Ser Met Glu Lys Asp Ala Phe Leu Phe Met Arg Asn Leu Lys	
1 5 10 15	
Val Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu	
20 25 30	
Pro Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys	
35 40 45	
Ile Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Xaa Leu Asp	
50 55 60	
Leu Xaa Gly Asn Cys Pro Arg Cys Xaa Asn Val Pro Tyr Pro Cys Thr	
65 70 75 80	
Pro Cys Glu Asn Asn Ser Pro Leu Gln Ile His Xaa Asn Ala Phe Asn	
85 90 95	
Ser Ser Thr Xaa	
100	

<210> 29  
 <211> 1756  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:rodent; surmised  
 Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(1182)

<400> 29  
 tct cca gaa att ccc tgg aat tcc ttg cct cct gag gtt ttt gag ggt 48  
 Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly  
 1 5 10 15  
 atg ccg cca aat cta aag aat ctc tcc ttg gcc aaa aat ggg ctc aaa 96  
 Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys  
 20 25 30  
 tct ttc ttt tgg gac aga ctc cag tta ctg aag cat ttg gaa att ttg 144  
 Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu  
 35 40 45  
 gag ctc agc cat aac cag ctg aca aaa gta cct gag aga ttg gcc aac 192  
 Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn  
 50 55 60  
 tgg tcc aaa agt ctc aca aca ctg att ctt aag cat aat caa atc agg 240  
 Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg  
 65 70 75 80  
 caa ttg aca aaa tat ttt cta gaa gat gct ttg caa ttg cgc tat cta 288  
 Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu  
 85 90 95  
 gag atc agt tca aat aaa atc cag gtc att cag aag act agc ttc cca 336  
 Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro  
 100 105 110  
 gaa aat gtc ctc aac aat ctg gag atg ttg gtt tta cat cac aat cgc 384  
 Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg  
 115 120 125  
 ttt ctt tgc aac tgt gat gct gtg tgg ttt gtc tgg tgg gtt aac cat 432  
 Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His  
 130 135 140  
 aca gat gtt act att cca tac ctg gcc act gat gtg act tgt gta ggt 480  
 Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly  
 145 150 155 160  
 cca gga gca cac aaa ggt caa agt gtc ata tcc ctt gat ctg tat acg 528  
 Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr  
 165 170 175

tgt gag tta gat ctc aca aac ctg att ctg ttc tca gtt tcc ata tca	576
Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser	
180 185 190	
tca gtc ctc ttt ctt atg gta gtt atg aca aca agt cac ctc ttt ttc	624
Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe	
195 200 205	
tgg gat atg tgg tac att tat tat ttt tgg aaa gca aag ata aag ggg	672
Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly	
210 215 220	
tat cca gca tct gca atc cca tgg agt cct tgt tat gat gct ttt att	720
Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile	
225 230 235 240	
gtg tat gac act aaa aac tca gct gtg aca gaa tgg gtt ttg cag gag	768
Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu	
245 250 255	
ctg gtg gca aaa ttg gaa gat cca aga gaa aaa cac ttc aat ttg tgt	816
Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys	
260 265 270	
ctg gaa gaa aga gac tgg cta cca gga cag cca gtt cta gaa aac ctt	864
Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu	
275 280 285	
tct cag agc ata cag ctc agc aaa aag aca gtg ttt gtg atg aca cag	912
Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln	
290 295 300	
aaa tat gct aag act gag agt ttt aag atg gca ttt tat ttg tct cat	960
Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His	
305 310 315 320	
cag agg ctc ctg gat gaa aaa gtg gat gtg att atc ttg ata ttc ttg	1008
Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu	
325 330 335	
gaa aga cct ctt cag aag tct aag ttt ctt cag ctc agg aag aga ctc	1056
Glu Arg Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu	
340 345 350	
tgc agg agc tct gtc ctt gag tgg cct gca aat cca cag gct cac cca	1104
Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His Pro	
355 360 365	
tac ttc tgg cag tgc ctg aaa aat gcc ctg acc aca gac aat cat gtg	1152
Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His Val	
370 375 380	
gct tat agt caa atg ttc aag gaa aca gtc tagctctctg aagaatgtca	1202
Ala Tyr Ser Gln Met Phe Lys Glu Thr Val	

385

390

ccacctagga catgccttgg tacctgaagt tttcataaag gtttccataa atgaagggtct 1262  
 gaatttttcc taacagttgt catggctcag attggtggga aatcatcaat atatggctaa 1322  
 gaaattaaga aggggagact gatagaagat aatttctttc ttcattgtgcc atgctcagtt 1382  
 aaatatttcc cctagctcaa atctgaaaaa ctgtgcctag gagacaacac aaggctttga 1442  
 tttatctgca tacaattgat aagagccaca catctgccct gaagaagtac tagtagtttt 1502  
 agtagtaggg taaaaattac acaagctttc tctctctctg atactgaact gtaccagagt 1562  
 tcaatgaaat aaaagcccag agaacttctc agtaaattgg ttcattatca ttagtagtatcc 1622  
 accatgcaat atgccacaaa rccgctactg gtacaggaca gntggtagct gcttcaakgc 1682  
 ctcttatcat tttcttgggg cccatggagg ggttctytgg gaaadaggga agkttttttt 1742  
 1756  
 tggccatcca tgaa

&lt;210&gt; 30

&lt;211&gt; 394

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;400&gt; 30

Ser Pro Glu Ile Pro Trp Asn Ser Leu Pro Pro Glu Val Phe Glu Gly  
 1 5 10 15

Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys  
 20 25 30

Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile Leu  
 35 40 45

Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala Asn  
 50 55 60

Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile Arg  
 65 70 75 80

Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr Leu  
 85 90 95

Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe Pro  
 100 105 110

Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn Arg  
 115 120 125

Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn His  
 130 135 140  
 Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val Gly  
 145 150 155 160  
 Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr Thr  
 165 170 175  
 Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile Ser  
 180 185 190  
 Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe Phe  
 195 200 205  
 Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys Gly  
 210 215 220  
 Tyr Pro Ala Ser Ala Ile Pro Trp Ser Pro Cys Tyr Asp Ala Phe Ile  
 225 230 235 240  
 Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu  
 245 250 255  
 Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys  
 260 265 270  
 Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu  
 275 280 285  
 Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln  
 290 295 300  
 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His  
 305 310 315 320  
 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu  
 325 330 335  
 Glu Arg Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu  
 340 345 350  
 Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His Pro  
 355 360 365  
 Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn His Val  
 370 375 380  
 Ala Tyr Ser Gln Met Phe Lys Glu Thr Val  
 385 390

<210> 31  
 <211> 999

<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (2)..(847)

<220>  
<221> misc\_feature  
<222> (1)..(282)  
<223> Xaa translation depends on genetic code

<400> 31  
c tcn gat gcc aag att cgg cac nag gca tat tca gag gtc atg atg gtt 49  
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val  
1 5 10 15  
ggc tgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga 97  
Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly  
20 25 30  
acc agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct 145  
Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala  
35 40 45  
ctg ttg att gtc acc att gtg gtt att atg cta gtt ctg ggg ttg gct 193  
Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala  
50 55 60  
gtg gcc ttc tgc tgt ctc cac ttt gat ctg ccc tgg tat ctc agg atg 241  
Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met  
65 70 75 80  
cta ggt caa tgc aca caa aca tgg cac agg gtt agg aaa aca acc caa 289  
Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln  
85 90 95  
gaa caa ctc aag aga aat gtc cga ttc cac gca ttt att tca tac agt 337  
Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser  
100 105 110  
gaa cat gat tct ctg tgg gtg aag aat gaa ttg atc ccc aat cta gag 385  
Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu  
115 120 125  
aag gaa gat ggt tct atc ttg att tgc ctt tat gaa agc tac ttt gac 433  
Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp  
130 135 140

cct ggc aaa agc att agt gaa aat att gta agc ttc att gag aaa agc 481  
Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser 160  
145 150 155

tat aag tcc atc ttt gtt ttg tct ccc aac ttt gtc cag aat gag tgg 529  
Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp 175  
165 170

tgc cat tat gaa ttc tac ttt gcc cac cac aat ctc ttc cat gaa aat 577  
Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn 190  
180 185

tct gat cac ata att ctt atc tta ctg gaa ccc att cca ttc tat tgc 625  
Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys 205  
195 200

att ccc acc agg tat cat aaa ctg raa gct ctc ctg gaa aaa aaa gca 673  
Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala 220  
210 215

tac ttg gaa tgg ccc aag gat agg cgt aaa tgt ggg ctt tty tgg gca 721  
Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala 240  
225 230 235

aae ctt cga gct gct gtt aat gtt aat gta tta gcc acc aga gaa atg 769  
Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met 255  
245 250

tat gaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct 817  
Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser 270  
260 265

aga atc tyt ctg atg aga aca gac tgt yta taaaatccca cagtccttgg 867  
Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa 280  
275

gaagttgggg accacataca ctggttgggat gtacattgat acaaccttta tgatggcaat 927  
ttgacaatat ttattaaaat aaaaaatggt tattcccttc aaaaaaaaaa aaaaaaaaaa 987  
aaaaaaaaaa aa 999

<210> 32  
<211> 282  
<212> PRT  
<213> Unknown

<400> 32  
Xaa Asp Ala Lys Ile Arg His Xaa Ala Tyr Ser Glu Val Met Met Val  
1 5 10 15

Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly  
20 25 30

Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr Ala  
 35 40 45  
 Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala  
 50 55 60  
 Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg Met  
 65 70 75 80  
 Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln  
 85 90 95  
 Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser  
 100 105 110  
 Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu  
 115 120 125  
 Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp  
 130 135 140  
 Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser  
 145 150 155 160  
 Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp  
 165 170 175  
 Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu Asn  
 180 185 190  
 Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys  
 195 200 205  
 Ile Pro Thr Arg Tyr His Lys Leu Xaa Ala Leu Leu Glu Lys Lys Ala  
 210 215 220  
 Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Xaa Trp Ala  
 225 230 235 240  
 Asn Leu Arg Ala Ala Val Asn Val Asn Val Leu Ala Thr Arg Glu Met  
 245 250 255  
 Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser  
 260 265 270  
 Thr Ile Xaa Leu Met Arg Thr Asp Cys Xaa  
 275 280

<210> 33  
 <211> 1173  
 <212> DNA



<213> Unknown

<220>

<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>

<221> CDS

<222> (1)..(1008)

<220>

<221> misc feature

<222> (285)

<223> Xaa translation depends on genetic code

<400> 33  
ctg cct gct ggc acc cgg ctc cgg agg ctg gat gtc agc tgc aac agc 48  
Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser  
1 5 10 15  
atc agc ttc gtg gcc ccc ggc ttc ttt tcc aag gcc aag gag ctg cga 96  
Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg  
20 25 30  
gag ctc aac ctt agc gcc aac gcc ctc aag aca gtg gac cac tcc tgg 144  
Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp  
35 40 45  
ttt ggg ccc ctg gcg agt gcc ctg caa ata cta gat gta agc gcc aac 192  
Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn  
50 55 60  
cct ctg cac tgc gcc tgt ggg gcg gcc ttt atg gac ttc ctg ctg gag 240  
Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu  
65 70 75 80  
gtg cag gct gcc gtg ccc ggt ctg ccc agc cgg gtg aag tgt ggc agt 288  
Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser  
85 90 95  
ccg ggc cag ctc cag ggc ctc agc atc ttt gca cag gac ctg cgc ctc 336  
Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu  
100 105 110  
tgc ctg gat gag gcc ctc tcc tgg gac tgt ttc gcc ctc tcg ctg ctg 384  
Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu  
115 120 125  
gct gtg gct ctg ggc ctg ggt gtg ccc atg ctg cat cac ctc tgt ggc 432  
Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly  
130 135 140  
tgg gac ctc tgg tac tgc ttc cac ctg tgc ctg gcc tgg ctt ccc tgg 480  
Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp

145	150	155	160	
cgg ggg cgg caa agt ggg cga gat gag gat gcc ctg ccc tac gat gcc				528
Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala				
	165	170	175	
ttc gtg gtc ttc gac aaa acg cag agc gca gtg gca gac tgg gtg tac				576
Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr				
	180	185	190	
aac gag ctt cgg ggg cag ctg gag gag tgc cgt ggg cgc tgg gca ctc				624
Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu				
	195	200	205	
cgc ctg tgc ctg gag gaa cgc gac tgg ctg cct ggc aaa acc ctc ttt				672
Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe				
	210	215	220	
gag aac ctg tgg gcc tcg gtc tat ggc agc cgc aag acg ctg ttt gtg				720
Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val				
	225	230	235	
ctg gcc cac acg gac cgg gtc agt ggt ctc ttg cgc gcc agc ttc ctg				768
Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu				
	245	250	255	
ctg gcc cag cag cgc ctg ctg gag gac cgc aag gac gtc gtg gtg ctg				816
Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu				
	260	265	270	
gtg atc ctg agc cct gac ggc cgc cgc tcc cgc tac gkg cgg ctg cgc				864
Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg				
	275	280	285	
cag cgc ctc tgc cgc cag agt gtc ctc ctc tgg ccc cac cag ccc agt				912
Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser				
	290	295	300	
ggt cag cgc agc ttc tgg gcc cag ctg ggc atg gcc ctg acc agg gac				960
Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp				
	305	310	315	
aac cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa				1008
Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu				
	325	330	335	
tagccgtgag ccggaatcct gcacggtgcc acctccacac tcacctcacc tctgcctgcc				1068
tggtctgacc ctcccctgct cgcctccctc accccacacc tgacacagag caggcactca				1128
ataaatgcta ccgaaggcta aaaaaaaaaa aaaaaaaaaa aanna				1173

<210> 34  
<211> 336  
<212> PRT  
<213> Unknown

<400> 34  
Leu Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser  
1 5 10 15

Ile Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg  
20 25 30

Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp  
35 40 45

Phe Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn  
50 55 60

Pro Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu  
65 70 75 80

Val Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser  
85 90 95

Pro Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu  
100 105 110

Cys Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu  
115 120 125

Ala Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly  
130 135 140

Trp Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp  
145 150 155 160

Arg Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala  
165 170 175

Phe Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr  
180 185 190

Asn Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu  
195 200 205

Arg Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe  
210 215 220

Glu Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val  
225 230 235 240

Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu  
245 250 255

Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu  
 260 265 270  
 Val Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Xaa Arg Leu Arg  
 275 280 285  
 Gln Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser  
 290 295 300  
 Gly Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp  
 305 310 315 320  
 Asn His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu  
 325 330 335

<210> 35  
 <211> 497  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:rodent; surmised  
 Mus musculus

<400> 35  
 tggccacac ggaccgcgtc agtggcctcc tgcgcaccag cttcctgctg gctcagcagc 60  
 gcctgttgga agaccgcaag gacgtggtgg tggttggtgat cctgcgctccg gatgccccac 120  
 cgtcccgcta tgtgcgactg cgccagcgtc tctgccgcca gagtgtgctc ttctggcccc 180  
 agcgacccaa cgggcagggg ggcttctggg ccagctgag tacagccctg actagggaca 240  
 accgccactt ctataaccag aacttctgcc ggggacctac agcagaatag ctgagagcaa 300  
 cagctggaaa cagctgcctc ttcattgtctg gttcccgagt tgctctgcct gccttgctct 360  
 gtcttactac accgctatct ggcaagtgcg caatatatgc taccaagcca ccaggccac 420  
 ggagcaaagg ttggctgtaa agggtagttt tcttcccatg catctttcag gagagtgaag 480  
 atagacacca aaccac 497

<210> 36  
 <211> 3099  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism:primate; surmised  
 Homo sapiens

<220>  
<221> CDS  
<222> (1)..(3096)

<220>  
<221> mat\_peptide  
<222> (52)..(3096)

<220>  
<221> misc\_feature  
<222> (725)  
<223> Xaa translation depends on genetic code

<400> 36  
atg ctg acc tgc att ttc ctg cta ata tct ggt tcc tgt gag tta tgc 48  
Met Leu Thr Cys Ile Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys  
-15 -10 -5

gcc gaa gaa aat ttt tct aga agc tat cct tgt gat gag aaa aag caa 96  
Ala Glu Glu Asn Phe Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln  
-1 5 10 15

aat gac tca gtt att gca gag tgc agc aat cgt cga cta cag gaa gtt 144  
Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val  
20 25 30

ccc caa acg gtg ggc aaa tat gtg aca gaa cta gac ctg tct gat aat 192  
Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn  
35 40 45

ttc atc aca cac ata acg aat gaa tca ttt caa ggg ctg caa aat ctc 240  
Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu  
50 55 60

act aaa ata aat cta aac cac aac ccc aat gta cag cac cag aac gga 288  
Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
65 70 75

aat ccc ggt ata caa tca aat ggc ttg aat atc aca gac ggg gca ttc 336  
Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe  
80 85 90 95

ctc aac cta aaa aac cta agg gag tta ctg ctt gaa gac aac cag tta 384  
Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu  
100 105 110

ccc caa ata ccc tct ggt ttg cca gag tct ttg aca gaa ctt agt cta 432  
Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu  
115 120 125

att caa aac aat ata tac aac ata act aaa gag ggc att tca aga ctt 480  
Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu  
130 135 140

aa aac ttg aaa aat ctc tat ttg gcc tgg aac tgc tat ttt aac aaa	528
le Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys	
145 150 155	
tt tgc gag aaa act aac ata gaa gat gga gta ttt gaa acg ctg aca	576
al Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr	
60 165 170 175	
at ttg gag ttg cta tca cta tct ttc aat tct ctt tca cat gtg cca	624
asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro	
180 185 190	
ccc aaa ctg cca agc tcc cta cgc aaa ctt ttt ctg agc aac acc cag	672
pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln	
195 200 205	
atc aaa tac att agt gaa gaa gat ttc aag gga ttg ata aat tta aca	720
ile Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr	
210 215 220	
tta cta gat tta agc ggg aac tgt ccg agg tgc ttc aat gcc cca ttt	768
Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe	
225 230 235	
cca tgc gtg cct tgt gat ggt ggt gct tca att aat ata gat cgt ttt	816
Pro Lys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe	
240 245 250 255	
gct ttt caa aac ttg acc caa ctt cga tac cta aac ctc tct agc act	864
Ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr	
260 265 270	
tcc ctc agg aag att aat gct gcc tgg ttt aaa aat atg cct cat ctg	912
Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu	
275 280 285	
aag gtg ctg gat ctt gaa ttc aac tat tta gtg gga gaa ata gcc tct	960
Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Ala Ser	
290 295 300	
ggg gca ttt tta acg atg ctg ccc cgc tta gaa ata ctt gac ttg tct	1008
Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	
305 310 315	
ttt aac tat ata aag ggg agt tat cca cag cat att aat att tcc aga	1056
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg	
320 325 330 335	
aac ttc tct aaa ctt ttg tct cta cgg gca ttg cat tta aga ggt tat	1104
Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr	
340 345 350	

g	ttc	cag	gaa	ctc	aga	gaa	gat	gat	ttc	cag	ccc	ctg	atg	cag	ctt	1152
al	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu	Met	Gln	Leu	
			355					360					365			
ca	aac	tta	tcg	act	atc	aac	ttg	ggt	att	aat	ttt	att	aag	caa	atc	1200
ro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe	Ile	Lys	Gln	Ile	
		370					375					380				
at	ttc	aaa	ctt	ttc	caa	aat	ttc	tcc	aat	ctg	gaa	att	att	tac	ttg	1248
sp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu	Glu	Ile	Ile	Tyr	Leu	
		385				390					395					
ca	gaa	aac	aga	ata	tca	ccg	ttg	gta	aaa	gat	acc	cgg	cag	agt	tat	1296
er	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys	Asp	Thr	Arg	Gln	Ser	Tyr	
00					405					410					415	
ca	aat	agt	tcc	tct	ttt	caa	cgt	cat	atc	cgg	aaa	cga	cgc	tca	aca	1344
ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His	Ile	Arg	Lys	Arg	Arg	Ser	Thr	
			420					425						430		
gat	ttt	gag	ttt	gac	cca	cat	tcg	aac	ttt	tat	cat	ttc	acc	cgt	cct	1392
Asp	Phe	Glu	Phe	Asp	Pro	His	Ser	Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	
			435					440					445			
tta	ata	aag	cca	caa	tgt	gct	gct	tat	gga	aaa	gcc	tta	gat	tta	agc	1440
Leu	Ile	Lys	Pro	Gln	Cys	Ala	Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	
		450					455					460				
ctc	aac	agt	att	ttc	ttc	att	ggg	cca	aac	caa	ttt	gaa	aat	ctt	cct	1488
Leu	Asn	Ser	Ile	Phe	Phe	Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	
		465				470					475					
gac	att	gcc	tgt	tta	aat	ctg	tct	gca	aat	agc	aat	gct	caa	gtg	tta	1536
Asp	Ile	Ala	Cys	Leu	Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	
480					485					490					495	
agt	gga	act	gaa	ttt	tca	gcc	att	cct	cat	gtc	aaa	tat	ttg	gat	ttg	1584
Ser	Gly	Thr	Glu	Phe	Ser	Ala	Ile	Pro	His	Val	Lys	Tyr	Leu	Asp	Leu	
			500						505					510		
aca	aac	aat	aga	cta	gac	ttt	gat	aat	gct	agt	gct	ctt	act	gaa	ttg	1632
Thr	Asn	Asn	Arg	Leu	Asp	Phe	Asp	Asn	Ala	Ser	Ala	Leu	Thr	Glu	Leu	
			515					520					525			
tcc	gac	ttg	gaa	gtt	cta	gat	ctc	agc	tat	aat	tca	cac	tat	ttc	aga	1680
Ser	Asp	Leu	Glu	Val	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	His	Tyr	Phe	Arg	
		530					535					540				
ata	gca	ggc	gta	aca	cat	cat	cta	gaa	ttt	att	caa	aat	ttc	aca	aat	1728
Ile	Ala	Gly	Val	Thr	His	His	Leu	Glu	Phe	Ile	Gln	Asn	Phe	Thr	Asn	
		545				550					555					
cta	aaa	gtt	tta	aac	ttg	agc	cac	aac	aac	att	tat	act	tta	aca	gat	1776
Leu	Lys	Val	Leu	Asn	Leu	Ser	His	Asn	Asn	Ile	Tyr	Thr	Leu	Thr	Asp	

560	565	570	575	
aag tat aac ctg gaa agc aag tcc ctg gta gaa tta gtt ttc agt ggc Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly 580 585 590				1824
aat cgc ctt gac att ttg tgg aat gat gat gac aac agg tat atc tcc Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser 595 600 605				1872
att ttc aaa ggt ctc aag aat ctg aca cgt ctg gat tta tcc ctt aat Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn 610 615 620				1920
agg ctc aag cac atc cca aat gaa gca ttc ctt aat ttg cca gcg agt Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser 625 630 635				1968
ctc act gaa cta cat ata aat gat aat atg tta aag ttt ttt aac tgg Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp 640 645 650 655				2016
aca tta ctc cag cag ttt cct cgt ctc gag ttg ctt gac tta cgt gga Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly 660 665 670				2064
aac aaa cta ctc ttt tta act gat agc cta tct gac ttt aca tct tcc Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser 675 680 685				2112
ctt cgg aca ctg ctg ctg agt cat aac agg att tcc cac cta ccc tct Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser 690 695 700				2160
ggc ttt ctt tct gaa gtc agt agt ctg aag cac ctc gat tta agt tcc Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser 705 710 715				2208
aat ctg cta aaa aca atm aac aaa tcc gca ctt gaa act aag acc acc Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr 720 725 730 735				2256
acc aaa tta tct atg ttg gaa cta cac gga aac ccc ttt gaa tgc acc Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr 740 745 750				2304
tgt gac att gga gat ttc cga aga tgg atg gat gaa cat ctg aat gtc Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val 755 760 765				2352
aaa att ccc aga ctg gta gat gtc att tgt gcc agt cct ggg gat caa Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln 770 775 780				2400



aga ggg aag agt att gtg agt ctg gag cta aca act tgt gtt tca gat	2448
Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	
785 790 795	
gtc act gca gtg ata tta ttt ttc ttc acg ttc ttt atc acc acc atg	2496
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met	
800 805 810 815	
gtt atg ttg gct gcc ctg gct cac cat ttg ttt tac tgg gat gtt tgg	2544
Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp	
820 825 830	
ttt ata tat aat gtg tgt tta gct aag tta aaa ggc tac agg tct ctt	2592
Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu	
835 840 845	
tcc aca tcc caa act ttc tat gat gct tac att tct tat gac acc aaa	2640
Ser Thr Ser Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys	
850 855 860	
gat gcc tct gtt act gac tgg gtg ata aat gag ctg cgc tac cac ctt	2688
Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu	
865 870 875	
gaa gag agc cga gac aaa aac gtt ctc ctt tgt cta gag gag agg gat	2736
Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp	
880 885 890 895	
tgg gac ccg gga ttg gcc atc atc gac aac ctc atg cag agc atc aac	2784
Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn	
900 905 910	
caa agc aag aaa aca gta ttt gtt tta acc aaa aaa tat gca aaa agc	2832
Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser	
915 920 925	
tgg aac ttt aaa aca gct ttt tac ttg gcc ttg cag agg cta atg ggt	2880
Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly	
930 935 940	
gag aac atg gat gtg att ata ttt atc ctg ctg gag cca gtg tta cag	2928
Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln	
945 950 955	
cat tct ccg tat ttg agg cta cgg cag cgg atc tgt aag agc tcc atc	2976
His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile	
960 965 970 975	
ctc cag tgg cct gac aac ccg aag gca gaa ggc ttg ttt tgg caa act	3024
Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr	
980 985 990	
ctg aga aat gtg gtc ttg act gaa aat gat tca cgg tat aac aat atg	3072

eu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met  
995 1000 1005

3099

at gtc gat tcc att aag caa tac taa  
yr Val Asp Ser Ile Lys Gln Tyr  
1010 1015

210> 37  
211> 1032  
212> PRT  
213> Unknown

400> 37  
Met Leu Thr Cys Ile Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys  
-15 -10 -5

Ala Glu Glu Asn Phe Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln  
-1 1 5 10 15

Asn Asp Ser Val Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val  
20 25 30

Pro Gln Thr Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn  
35 40 45

Phe Ile Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu  
50 55 60

Thr Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
65 70 75

Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe  
80 85 90 95

Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu  
100 105 110

Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu  
115 120 125

Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu  
130 135 140

Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys  
145 150 155

Val Cys Glu Lys Thr Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr  
160 165 170 175

Asn Leu Glu Leu Leu Ser Leu Ser Phe Asn Ser Leu Ser His Val Pro  
180 185 190

ro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln  
 195 200 205  
 le Lys Tyr Ile Ser Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr  
 210 215 220  
 leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe  
 225 230 235  
 pro Cys Val Pro Cys Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe  
 240 245 250 255  
 ala Phe Gln Asn Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr  
 260 265 270  
 Ser Leu Arg Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu  
 275 280 285  
 Lys Val Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Ala Ser  
 290 295 300  
 Gly Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser  
 305 310 315  
 Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg  
 320 325 330 335  
 Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr  
 340 345 350  
 Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu Met Gln Leu  
 355 360 365  
 Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile  
 370 375 380  
 Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu Glu Ile Ile Tyr Leu  
 385 390 395  
 Ser Glu Asn Arg Ile Ser Pro Leu Val Lys Asp Thr Arg Gln Ser Tyr  
 400 405 410 415  
 Ala Asn Ser Ser Ser Phe Gln Arg His Ile Arg Lys Arg Arg Ser Thr  
 420 425 430  
 Asp Phe Glu Phe Asp Pro His Ser Asn Phe Tyr His Phe Thr Arg Pro  
 435 440 445  
 Leu Ile Lys Pro Gln Cys Ala Ala Tyr Gly Lys Ala Leu Asp Leu Ser  
 450 455 460  
 Leu Asn Ser Ile Phe Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro  
 465 470 475

Asp Ile Ala Cys Leu Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu  
 180 485 490 495  
 Ser Gly Thr Glu Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu  
 500 505 510  
 Thr Asn Asn Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu  
 515 520 525  
 Ser Asp Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg  
 530 535 540  
 Ile Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
 545 550 555  
 Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr Asp  
 560 565 570 575  
 Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly  
 580 585 590  
 Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser  
 595 600 605  
 Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn  
 610 615 620  
 Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser  
 625 630 635  
 Leu Thr Glu Leu His Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp  
 640 645 650 655  
 Thr Leu Leu Gln Gln Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly  
 660 665 670  
 Asn Lys Leu Leu Phe Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser  
 675 680 685  
 Leu Arg Thr Leu Leu Leu Ser His Asn Arg Ile Ser His Leu Pro Ser  
 690 695 700  
 Gly Phe Leu Ser Glu Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser  
 705 710 715  
 Asn Leu Leu Lys Thr Xaa Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr  
 720 725 730 735  
 Thr Lys Leu Ser Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr  
 740 745 750  
 Cys Asp Ile Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val  
 755 760 765

Lys Ile Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln  
 770 775 780  
 Arg Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp  
 785 790 795  
 Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met  
 800 805 810 815  
 Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp Val Trp  
 820 825 830  
 Phe Ile Tyr Asn Val Cys Leu Ala Lys Leu Lys Gly Tyr Arg Ser Leu  
 835 840 845  
 Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys  
 850 855 860  
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu  
 865 870 875  
 Glu Glu Ser Arg Asp Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp  
 880 885 890 895  
 Trp Asp Pro Gly Leu Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn  
 900 905 910  
 Gln Ser Lys Lys Thr Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser  
 915 920 925  
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Gly  
 930 935 940  
 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln  
 945 950 955  
 His Ser Pro Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile  
 960 965 970 975  
 Leu Gln Trp Pro Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr  
 980 985 990  
 Leu Arg Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met  
 995 1000 1005  
 Tyr Val Asp Ser Ile Lys Gln Tyr  
 1010 1015

<210> 38  
 <211> 3046  
 <212> DNA  
 <213> Unknown

220>  
223> Description of Unknown Organism:primate; surmised  
Homo sapiens

220>  
221> CDS  
222> (111)..(2543)

220>  
221> mat\_peptide  
222> (168)..(2543)

400> 38  
aatcatcca cgcacctgca gctctgctga gagagtgcaa gccgtggggg ttttgagctc 60  
ttcttcatca ttcatatgag gaaataagtg gtaaaatcct tggaaataca atg aga 116  
Met Arg  
ctc atc aga aac att tac ata ttt tgt agt att gtt atg aca gca gag 164  
Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu  
-15 -10 -5  
ggg gat gct cca gag ctg cca gaa gaa agg gaa ctg atg acc aac tgc 212  
Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr Asn Cys  
-1 1 5 10 15  
tcc aac atg tct cta aga aag gtt ccc gca gac ttg acc cca gcc aca 260  
Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr  
20 25 30  
acg aca ctg gat tta tcc tat aac ctc ctt ttt caa ctc cag agt tca 308  
Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln Ser Ser  
35 40 45  
gat ttt cat tct gtc tcc aaa ctg aga gtt ttg att cta tgc cat aac 356  
Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn  
50 55 60  
aga att caa cag ctg gat ctc aaa acc ttt gaa ttc aac aag gag tta 404  
Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys Glu Leu  
65 70 75  
aga tat tta gat ttg tct aat aac aga ctg aag agt gta act tgg tat 452  
Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr Trp Tyr  
80 85 90 95  
tta ctg gca ggt ctc agg tat tta gat ctt tct ttt aat gac ttt gac 500  
Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp  
100 105 110  
acc atg cct atc tgt gag gaa gct ggc aac atg tca cac ctg gaa atc 548  
Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile

115

120

125

cta ggt ttg agt ggg gca aaa ata caa aaa tca gat ttc cag aaa att 596  
 Leu Gly Leu Ser Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile  
 130 135 140

gct cat ctg cat cta aat act gtc ttc tta gga ttc aga act ctt cct 644  
 Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro  
 145 150 155

cat tat gaa gaa ggt agc ctg ccc atc tta aac aca aca aaa ctg cac 692  
 His Tyr Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His  
 160 165 170 175

att gtt tta cca atg gac aca aat ttc tgg gtt ctt ttg cgt gat gga 740  
 Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly  
 180 185 190

atc aag act tca aaa ata tta gaa atg aca aat ata gat ggc aaa agc 788  
 Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys Ser  
 195 200 205

caa ttt gta agt tat gaa atg caa cga aat ctt agt tta gaa aat gct 836  
 Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu Asn Ala  
 210 215 220

aag aca tcg gtt cta ttg ctt aat aaa gtt gat tta ctc tgg gac gac 884  
 Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp Asp Asp  
 225 230 235

ctc ttc ctt atc tta caa ttt gtt tgg cat aca tca gtg gaa cac ttt 932  
 Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser Val Glu His Phe  
 240 245 250 255

cag atc cga aat gtg act ttt ggt ggt aag gct tat ctt gac cac aat 980  
 Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp His Asn  
 260 265 270

tca ttt gac tac tca aat act gta atg aga act ata aaa ttg gag cat 1028  
 Ser Phe Asp Tyr Ser Asn Thr Val Met Arg Thr Ile Lys Leu Glu His  
 275 280 285

gta cat ttc aga gtg ttt tac att caa cag gat aaa atc tat ttg ctt 1076  
 Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr Leu Leu  
 290 295 300

ttg acc aaa atg gac ata gaa aac ctg aca ata tca aat gca caa atg 1124  
 Leu Thr Lys Met Asp Ile Glu Asn Leu Thr Ile Ser Asn Ala Gln Met  
 305 310 315

cca cac atg ctt ttc ccg aat tat cct acg aaa ttc caa tat tta aat 1172  
 Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr Leu Asn  
 320 325 330 335

ttt gcc aat aat atc tta aca gac gag ttg ttt aaa aga act atc caa	1220
Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln	
340 345 350	
ctg cct cac ttg aaa act ctc att ttg aat ggc aat aaa ctg gag aca	1268
Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr	
355 360 365	
ctt tct tta gta agt tgc ttt gct aac aac aca ccc ttg gaa cac ttg	1316
Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu	
370 375 380	
gat ctg agt caa aat cta tta caa cat aaa aat gat gaa aat tgc tca	1364
Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser	
385 390 395	
tgg cca gaa act gtg gtc aat atg aat ctg tca tac aat aaa ttg tct	1412
Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser	
400 405 410 415	
gat tct gtc ttc agg tgc ttg ccc aaa agt att caa ata ctt gac cta	1460
Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu	
420 425 430	
aat aat aac caa atc caa act gta cct aaa gag act att cat ctg atg	1508
Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met	
435 440 445	
gca tta cga gaa cta aat att gca ttt aat ttt cta act gat ctc cct	1556
Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp Leu Pro	
450 455 460	
gga tgc agt cat ttc agt aga ctt tca gtt ctg aac att gaa atg aac	1604
Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn	
465 470 475	
ttc att ctc agc cca tct ctg gat ttt gtt cag agc tgc cag gaa gtt	1652
Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln Glu Val	
480 485 490 495	
aaa act cta aat gcg gga aga aat cca ttc cgg tgt acc tgt gaa tta	1700
Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu	
500 505 510	
aaa aat ttc att cag ctt gaa aca tat tca gag gtc atg atg gtt gga	1748
Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met Val Gly	
515 520 525	
tgg tca gat tca tac acc tgt gaa tac cct tta aac cta agg gga act	1796
Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr	
530 535 540	
agg tta aaa gac gtt cat ctc cac gaa tta tct tgc aac aca gct ctg	1844



Arg	Leu	Lys	Asp	Val	His	Leu	His	Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu		
545						550					555						
ttg	att	gtc	acc	att	gtg	ggt	att	atg	cta	ggt	ctg	ggg	ttg	gct	gtg	1892	
Leu	Ile	Val	Thr	Ile	Val	Val	Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val		
560					565					570					575		
gcc	ttc	tgc	tgt	ctc	cac	ttt	gat	ctg	ccc	tgg	tat	ctc	agg	atg	cta	1940	
Ala	Phe	Cys	Cys	Leu	His	Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu		
				580					585					590			
ggt	caa	tgc	aca	caa	aca	tgg	cac	agg	ggt	agg	aaa	aca	acc	caa	gaa	1988	
Gly	Gln	Cys	Thr	Gln	Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu		
			595					600					605				
caa	ctc	aag	aga	aat	gtc	cga	ttc	cac	gca	ttt	att	tca	tac	agt	gaa	2036	
Gln	Leu	Lys	Arg	Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu		
		610					615					620					
cat	gat	tct	ctg	tgg	gtg	aag	aat	gaa	ttg	atc	ccc	aat	cta	gag	aag	2084	
His	Asp	Ser	Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys		
						630					635						
gaa	gat	ggt	tct	atc	ttg	att	tgc	ctt	tat	gaa	agc	tac	ttt	gac	cct	2132	
Glu	Asp	Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro		
640					645					650					655		
ggc	aaa	agc	att	agt	gaa	aat	att	gta	agc	ttc	att	gag	aaa	agc	tat	2180	
Gly	Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr		
				660					665					670			
aag	tcc	atc	ttt	ggt	ttg	tct	ccc	aac	ttt	gtc	cag	aat	gag	tgg	tgc	2228	
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp	Cys		
			675					680					685				
cat	tat	gaa	ttc	tac	ttt	gcc	cac	cac	aat	ctc	ttc	cat	gaa	aat	tct	2276	
His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	Asn	Ser		
		690					695					700					
gat	cat	ata	att	ctt	atc	tta	ctg	gaa	ccc	att	cca	ttc	tat	tgc	att	2324	
Asp	His	Ile	Ile	Leu	Ile	Leu	Leu	Glu	Pro	Ile	Pro	Phe	Tyr	Cys	Ile		
						710					715						
ccc	acc	agg	tat	cat	aaa	ctg	aaa	gct	ctc	ctg	gaa	aaa	aaa	gca	tac	2372	
Pro	Thr	Arg	Tyr	His	Lys	Leu	Lys	Ala	Leu	Leu	Glu	Lys	Lys	Ala	Tyr		
720					725					730					735		
ttg	gaa	tgg	ccc	aag	gat	agg	cgt	aaa	tgt	ggg	ctt	ttc	tgg	gca	aac	2420	
Leu	Glu	Trp	Pro	Lys	Asp	Arg	Arg	Lys	Cys	Gly	Leu	Phe	Trp	Ala	Asn		
				740					745					750			
ctt	cga	gct	gct	att	aat	ggt	aat	gta	tta	gcc	acc	aga	gaa	atg	tat	2468	
Leu	Arg	Ala	Ala	Ile	Asn	Val	Asn	Val	Leu	Ala	Thr	Arg	Glu	Met	Tyr		
			755					760					765				

gaa ctg cag aca ttc aca gag tta aat gaa gag tct cga ggt tct aca 2516  
 Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser Thr  
 770 775 780

atc tct ctg atg aga aca gat tgt cta taaaatccca cagtccttgg 2563  
 Ile Ser Leu Met Arg Thr Asp Cys Leu  
 785 790

gaagttgggg accacataca ctgttgggat gtacattgat acaaccttta tgatggcaat 2623  
 ttgacaatat ttattaaaat aaaaaatggt tattcccttc atatcagttt ctagaaggat 2683  
 ttctaagaat gtatcctata gaaacacctt cacaagttaa taagggctta tggaaaaagg 2743  
 tggttcacccc aggattgttt ataatcatga aaaatgtggc caggtgcagt ggctcactct 2803  
 tgtaatccca gcactatggg aggccaagggt gggtgacca cgaggtcaag agatggagac 2863  
 catcctggcc aacatgggtga aaccctgtct ctactaaaaa taaaaaatt agctgggcgt 2923  
 gatcgtgcac gcctgtagtc ccagctactt gggaggctga ggcaggagaa tcgcttgaac 2983  
 ccgggaggtg gcagttgcag tgagctgaga tcgagccact gcactccagc ctggtgacag 3043  
 agc 3046

<210> 39  
 <211> 811  
 <212> PRT  
 <213> Unknown

<400> 39  
 Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr  
 -15 -10 -5

Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu Met Thr  
 -1 1 5 10

Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro  
 15 20 25

Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln  
 30 35 40 45

Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys  
 50 55 60

His Asn Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys  
 65 70 75

Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr

80

85

90

Trp Tyr Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp  
 95 100 105  
 Phe Asp Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu  
 110 115 120 125  
 Glu Ile Leu Gly Leu Ser Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln  
 130 135 140  
 Lys Ile Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr  
 145 150 155  
 Leu Pro His Tyr Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys  
 160 165 170  
 Leu His Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg  
 175 180 185  
 Asp Gly Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly  
 190 195 200 205  
 Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu  
 210 215 220  
 Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp  
 225 230 235  
 Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser Val Glu  
 240 245 250  
 His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp  
 255 260 265  
 His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg Thr Ile Lys Leu  
 270 275 280 285  
 Glu His Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr  
 290 295 300  
 Leu Leu Leu Thr Lys Met Asp Ile Glu Asn Leu Thr Ile Ser Asn Ala  
 305 310 315  
 Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr  
 320 325 330  
 Leu Asn Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr  
 335 340 345  
 Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu  
 350 355 360 365  
 Glu Thr Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu

370

375

380

His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn  
 385 390 395  
 Cys Ser Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys  
 400 405 410  
 Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu  
 415 420 425  
 Asp Leu Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His  
 430 435 440 445  
 Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp  
 450 455 460  
 Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu  
 465 470 475  
 Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln  
 480 485 490  
 Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys  
 495 500 505  
 Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met  
 510 515 520 525  
 Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg  
 530 535 540  
 Gly Thr Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr  
 545 550 555  
 Ala Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu  
 560 565 570  
 Ala Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg  
 575 580 585  
 Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr  
 590 595 600 605  
 Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr  
 610 615 620  
 Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu  
 625 630 635  
 Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe  
 640 645 650

Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys  
655 660 665

Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu  
670 675 680 685

Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu  
690 695 700

Asn Ser Asp His Ile Ile Leu Ile Leu Glu Pro Ile Pro Phe Tyr  
705 710 715

Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu Lys Lys  
720 725 730

Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp  
735 740 745

Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu Ala Thr Arg Glu  
750 755 760 765

Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly  
770 775 780

Ser Thr Ile Ser Leu Met Arg Thr Asp Cys Leu  
785 790

<210> 40  
<211> 2760  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (68)..(2455)

<220>  
<221> mat\_peptide  
<222> (161)..(2455)

<220>  
<221> misc\_feature  
<222> (2529)  
<223> n may be a, c, g, or t

<400> 40  
aagaatttgg actcatatca agatgctctg aagaagaaca accctttagg atagccactg 60  
caacatc atg acc aaa gac aaa gaa cct att gtt aaa agc ttc cat ttt 109

Met Thr Lys Asp Lys Glu Pro Ile Val Lys Ser Phe His Phe  
 -30 -25 -20

gtt tgc ctt atg atc ata ata gtt gga acc aga atc cag ttc tcc gac	157
Val Cys Leu Met Ile Ile Ile Val Gly Thr Arg Ile Gln Phe Ser Asp	
-15 -10 -5	
gga aat gaa ttt gca gta gac aag tca aaa aga ggt ctt att cat gtt	205
Gly Asn Glu Phe Ala Val Asp Lys Ser Lys Arg Gly Leu Ile His Val	
-1 1 5 10 15	
cca aaa gac cta ccg ctg aaa acc aaa gtc tta gat atg tct cag aac	253
Pro Lys Asp Leu Pro Leu Lys Thr Lys Val Leu Asp Met Ser Gln Asn	
20 25 30	
tac atc gct gag ctt cag gtc tct gac atg agc ttt cta tca gag ttg	301
Tyr Ile Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu	
35 40 45	
aca gtt ttg aga ctt tcc cat aac aga atc cag cta ctt gat tta agt	349
Thr Val Leu Arg Leu Ser His Asn Arg Ile Gln Leu Leu Asp Leu Ser	
50 55 60	
gtt ttc aag ttc aac cag gat tta gaa tat ttg gat tta tct cat aat	397
Val Phe Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn	
65 70 75	
cag ttg caa aag ata tcc tgc cat cct att gtg agt ttc agg cat tta	445
Gln Leu Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu	
80 85 90 95	
gat ttc tca ttc aat gat ttc aag gcc ctg ccc atc tgt aag gaa ttt	493
Asp Leu Ser Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe	
100 105 110	
ggc aac tta tca caa ctg aat ttc ttg gga ttg agt gct atg aag ctg	541
Gly Asn Leu Ser Gln Leu Asn Phe Leu Gly Leu Ser Ala Met Lys Leu	
115 120 125	
caa aaa tta gat ttg ctg cca att gct cac ttg cat cta agt tat atc	589
Gln Lys Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile	
130 135 140	
ctt ctg gat tta aga aat tat tat ata aaa gaa aat gag aca gaa agt	637
Leu Leu Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu Ser	
145 150 155	
cta caa att ctg aat gca aaa acc ctt cac ctt gtt ttt cac cca act	685
Leu Gln Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His Pro Thr	
160 165 170 175	
agt tta ttc gct atc caa gtg aac ata tca gtt aat act tta ggg tgc	733
Ser Leu Phe Ala Ile Gln Val Asn Ile Ser Val Asn Thr Leu Gly Cys	

180										185					190					
ta	caa	ctg	act	aat	att	aaa	ttg	aat	gat	gac	aac	tgt	caa	ggt	ttc	781				
Leu	Gln	Leu	Thr	Asn	Ile	Lys	Leu	Asn	Asp	Asp	Asn	Cys	Gln	Val	Phe					
			195					200					205							
att	aaa	ttt	tta	tca	gaa	ctc	acc	aga	ggt	cca	acc	tta	ctg	aat	ttt	829				
Ile	Lys	Phe	Leu	Ser	Glu	Leu	Thr	Arg	Gly	Pro	Thr	Leu	Leu	Asn	Phe					
		210					215					220								
acc	ctc	aac	cac	ata	gaa	acg	act	tgg	aaa	tgc	ctg	gtc	aga	gtc	ttt	877				
Thr	Leu	Asn	His	Ile	Glu	Thr	Thr	Trp	Lys	Cys	Leu	Val	Arg	Val	Phe					
		225				230					235									
caa	ttt	ctt	tgg	ccc	aaa	cct	gtg	gaa	tat	ctc	aat	att	tac	aat	tta	925				
Gln	Phe	Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu					
240					245					250					255					
aca	ata	att	gaa	agc	att	cgt	gaa	gaa	gat	ttt	act	tat	tct	aaa	acg	973				
Thr	Ile	Ile	Glu	Ser	Ile	Arg	Glu	Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr					
				260					265					270						
aca	ttg	aaa	gca	ttg	aca	ata	gaa	cat	atc	acg	aac	caa	ggt	ttt	ctg	1021				
Thr	Leu	Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu					
			275					280					285							
ttt	tca	cag	aca	gct	ttg	tac	acc	gtg	ttt	tct	gag	atg	aac	att	atg	1069				
Phe	Ser	Gln	Thr	Ala	Leu	Tyr	Thr	Val	Phe	Ser	Glu	Met	Asn	Ile	Met					
		290					295					300								
atg	tta	acc	att	tca	gat	aca	cct	ttt	ata	cac	atg	ctg	tgt	cct	cat	1117				
Met	Leu	Thr	Ile	Ser	Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His					
		305				310					315									
gca	tca	agc	aca	ttc	aag	ttt	ttg	aac	ttt	acc	cag	aac	ggt	ttc	aca	1165				
Ala	Pro	Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr					
320					325					330					335					
gat	agt	att	ttt	gaa	aaa	tgt	tcc	acg	tta	ggt	aaa	ttg	gag	aca	ctt	1213				
Asp	Ser	Ile	Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu					
				340					345					350						
atc	tta	caa	aag	aat	gga	tta	aaa	gac	ctt	ttc	aaa	gta	ggt	ctc	atg	1261				
Ile	Leu	Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met					
			355					360					365							
acg	aag	gat	atg	cct	tct	ttg	gaa	ata	ctg	gat	ggt	agc	tgg	aat	tct	1309				
Thr	Lys	Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser					
		370					375					380								
ttg	gaa	tct	ggt	aga	cat	aaa	gaa	aac	tgc	act	tgg	ggt	gag	agt	ata	1357				
Leu	Glu	Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile					
			385			390					395									

gtg	gtg	tta	aat	ttg	tct	tca	aat	atg	ctt	act	gac	tct	ggt	ttc	aga	1405
Val	Val	Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val	Phe	Arg	
400				405					410						415	
tgt	tta	cct	ccc	agg	atc	aag	gta	ctt	gat	ctt	cac	agc	aat	aaa	ata	1453
Cys	Leu	Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	
				420					425					430		
aag	agc	ggt	cct	aaa	caa	gtc	gta	aaa	ctg	gaa	gct	ttg	caa	gaa	ctc	1501
Lys	Ser	Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	
			435					440					445			
aat	ggt	gct	ttc	aat	tct	tta	act	gac	ctt	cct	gga	tgt	ggc	agc	ttt	1549
Asn	Val	Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	
		450					455					460				
agc	agc	ctt	tct	gta	ttg	atc	att	gat	cac	aat	tca	ggt	tcc	cac	cca	1597
Ser	Ser	Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	
		465				470					475					
tcg	ggt	gat	ttc	ttc	cag	agc	tgc	cag	aag	atg	agg	tca	ata	aaa	gca	1645
Ser	Ala	Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	
480					485					490					495	
ggg	gac	aat	cca	ttc	caa	tgt	acc	tgt	gag	cta	aga	gaa	ttt	gtc	aaa	1693
Gly	Asp	Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	
				500					505					510		
aat	ata	gac	caa	gta	tca	agt	gaa	gtg	tta	gag	ggc	tgg	cct	gat	tct	1741
Asn	Ile	Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	
			515					520					525			
tat	aag	tgt	gac	tac	cca	gaa	agt	tat	aga	gga	agc	cca	cta	aag	gac	1789
Tyr	Lys	Cys	Asp	Tyr	Pro	Glu	Ser	Tyr	Arg	Gly	Ser	Pro	Leu	Lys	Asp	
		530					535					540				
ttt	cac	atg	tct	gaa	tta	tcc	tgc	aac	ata	act	ctg	ctg	atc	gtc	acc	1837
Phe	His	Met	Ser	Glu	Leu	Ser	Cys	Asn	Ile	Thr	Leu	Leu	Ile	Val	Thr	
		545				550					555					
atc	ggt	gcc	acc	atg	ctg	gtg	ttg	gct	gtg	act	gtg	acc	tcc	ctc	tgc	1885
Ile	Gly	Ala	Thr	Met	Leu	Val	Leu	Ala	Val	Thr	Val	Thr	Ser	Leu	Cys	
560					565					570					575	
atc	tac	ttg	gat	ctg	ccc	tgg	tat	ctc	agg	atg	gtg	tgc	cag	tgg	acc	1933
Ile	Tyr	Leu	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Val	Cys	Gln	Trp	Thr	
				580					585					590		
cag	act	cgg	cgc	agg	gcc	agg	aac	ata	ccc	tta	gaa	gaa	ctc	caa	aga	1981
Gln	Thr	Arg	Arg	Arg	Ala	Arg	Asn	Ile	Pro	Leu	Glu	Glu	Leu	Gln	Arg	
			595				600						605			
aac	ctc	cag	ttt	cat	gct	ttt	att	tca	tat	agt	gaa	cat	gat	tct	gcc	2029



Asn	Leu	Gln	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser	Ala		
		610					615					620					
tgg	gtg	aaa	agt	gaa	ttg	gta	cct	tac	cta	gaa	aaa	gaa	gat	ata	cag	2077	
Trp	Val	Lys	Ser	Glu	Leu	Val	Pro	Tyr	Leu	Glu	Lys	Glu	Asp	Ile	Gln		
	625					630					635						
att	tgt	ctt	cat	gag	agg	aac	ttt	gtc	cct	ggc	aag	agc	att	gtg	gaa	2125	
Ile	Cys	Leu	His	Glu	Arg	Asn	Phe	Val	Pro	Gly	Lys	Ser	Ile	Val	Glu		
640					645					650					655		
aat	atc	atc	aac	tgc	att	gag	aag	agt	tac	aag	tcc	atc	ttt	gtt	ttg	2173	
Asn	Ile	Ile	Asn	Cys	Ile	Glu	Lys	Ser	Tyr	Lys	Ser	Ile	Phe	Val	Leu		
				660					665					670			
tct	ccc	aac	ttt	gtc	cag	agt	gag	tgg	tgc	cat	tac	gaa	ctc	tat	ttt	2221	
Ser	Pro	Asn	Phe	Val	Gln	Ser	Glu	Trp	Cys	His	Tyr	Glu	Leu	Tyr	Phe		
			675					680					685				
gcc	cat	cac	aat	ctc	ttt	cat	gaa	gga	tct	aat	aac	tta	atc	ctc	atc	2269	
Ala	His	His	Asn	Leu	Phe	His	Glu	Gly	Ser	Asn	Asn	Leu	Ile	Leu	Ile		
		690					695					700					
tta	ctg	gaa	ccc	att	cca	cag	aac	agc	att	ccc	aac	aag	tac	cac	aag	2317	
Leu	Leu	Glu	Pro	Ile	Pro	Gln	Asn	Ser	Ile	Pro	Asn	Lys	Tyr	His	Lys		
	705					710					715						
ctg	taag	gct	ctc	atg	acg	cag	cgg	act	tat	ttg	cag	tgg	ccc	aag	gag	2365	
Leu	Lys	Ala	Leu	Met	Thr	Gln	Arg	Thr	Tyr	Leu	Gln	Trp	Pro	Lys	Glu		
720					725					730					735		
aaa	agc	aaa	cgt	ggg	ctc	ttt	tgg	gct	aac	att	aga	gcc	gct	ttt	aat	2413	
Lys	Ser	Lys	Arg	Gly	Leu	Phe	Trp	Ala	Asn	Ile	Arg	Ala	Ala	Phe	Asn		
			740						745					750			
atg	aaa	tta	aca	cta	gtc	act	gaa	aac	aat	gat	gtg	aaa	tct			2455	
Met	Lys	Leu	Thr	Leu	Val	Thr	Glu	Asn	Asn	Asp	Val	Lys	Ser				
			755				760						765				
taaaaaaatt taggaaattc aacttaagaa accattatatt acttggatga tggatgaatag																	2515
tacagtcgta agtnactgtc tggaggtgcc tccattatcc tcatgccttc aggaaagact																	2575
taacaaaaaac aatgtttcat ctgggggaact gagctaggcg gtgaggttag cctgccagtt																	2635
agagacagcc cagtctcttc tggtttaatc attatgtttc aaattgaaac agtctctttt																	2695
gagtaaattgc tcagtttttc agtcctctc cactctgctt tcccaaattgg attctgttgg																	2755
tgaag																	2760

<210> 41  
<211> 796

<212> PRT  
<213> Unknown

<400> 41  
Met Thr Lys Asp Lys Glu Pro Ile Val Lys Ser Phe His Phe Val Cys  
-30 -25 -20

Leu Met Ile Ile Ile Val Gly Thr Arg Ile Gln Phe Ser Asp Gly Asn  
-15 -10 -5 -1 1

Glu Phe Ala Val Asp Lys Ser Lys Arg Gly Leu Ile His Val Pro Lys  
5 10 15

Asp Leu Pro Leu Lys Thr Lys Val Leu Asp Met Ser Gln Asn Tyr Ile  
20 25 30

Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu Thr Val  
35 40 45

Leu Arg Leu Ser His Asn Arg Ile Gln Leu Leu Asp Leu Ser Val Phe  
50 55 60 65

Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn Gln Leu  
70 75 80

Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu Asp Leu  
85 90 95

Ser Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe Gly Asn  
100 105 110

Leu Ser Gln Leu Asn Phe Leu Gly Leu Ser Ala Met Lys Leu Gln Lys  
115 120 125

Leu Asp Leu Leu Pro Ile Ala His Leu His Leu Ser Tyr Ile Leu Leu  
130 135 140 145

Asp Leu Arg Asn Tyr Tyr Ile Lys Glu Asn Glu Thr Glu Ser Leu Gln  
150 155 160

Ile Leu Asn Ala Lys Thr Leu His Leu Val Phe His Pro Thr Ser Leu  
165 170 175

Phe Ala Ile Gln Val Asn Ile Ser Val Asn Thr Leu Gly Cys Leu Gln  
180 185 190

Leu Thr Asn Ile Lys Leu Asn Asp Asp Asn Cys Gln Val Phe Ile Lys  
195 200 205

Phe Leu Ser Glu Leu Thr Arg Gly Pro Thr Leu Leu Asn Phe Thr Leu  
210 215 220 225

Asn His Ile Glu Thr Thr Trp Lys Cys Leu Val Arg Val Phe Gln Phe

230										235					240				
Leu	Trp	Pro	Lys	Pro	Val	Glu	Tyr	Leu	Asn	Ile	Tyr	Asn	Leu	Thr	Ile				
			245					250					255						
Ile	Glu	Ser	Ile	Arg	Glu	Glu	Asp	Phe	Thr	Tyr	Ser	Lys	Thr	Thr	Leu				
		260					265					270							
Lys	Ala	Leu	Thr	Ile	Glu	His	Ile	Thr	Asn	Gln	Val	Phe	Leu	Phe	Ser				
	275					280					285								
Gln	Thr	Ala	Leu	Tyr	Thr	Val	Phe	Ser	Glu	Met	Asn	Ile	Met	Met	Leu				
290					295					300									
Thr	Ile	Ser	Asp	Thr	Pro	Phe	Ile	His	Met	Leu	Cys	Pro	His	Ala	Pro				
				310					315					320					
Ser	Thr	Phe	Lys	Phe	Leu	Asn	Phe	Thr	Gln	Asn	Val	Phe	Thr	Asp	Ser				
			325					330					335						
Ile	Phe	Glu	Lys	Cys	Ser	Thr	Leu	Val	Lys	Leu	Glu	Thr	Leu	Ile	Leu				
	340						345					350							
Gln	Lys	Asn	Gly	Leu	Lys	Asp	Leu	Phe	Lys	Val	Gly	Leu	Met	Thr	Lys				
355						360					365								
Asp	Met	Pro	Ser	Leu	Glu	Ile	Leu	Asp	Val	Ser	Trp	Asn	Ser	Leu	Glu				
370					375					380					385				
Ser	Gly	Arg	His	Lys	Glu	Asn	Cys	Thr	Trp	Val	Glu	Ser	Ile	Val	Val				
				390					395					400					
Leu	Asn	Leu	Ser	Ser	Asn	Met	Leu	Thr	Asp	Ser	Val	Phe	Arg	Cys	Leu				
			405					410					415						
Pro	Pro	Arg	Ile	Lys	Val	Leu	Asp	Leu	His	Ser	Asn	Lys	Ile	Lys	Ser				
		420					425					430							
Val	Pro	Lys	Gln	Val	Val	Lys	Leu	Glu	Ala	Leu	Gln	Glu	Leu	Asn	Val				
		435				440					445								
Ala	Phe	Asn	Ser	Leu	Thr	Asp	Leu	Pro	Gly	Cys	Gly	Ser	Phe	Ser	Ser				
450					455					460					465				
Leu	Ser	Val	Leu	Ile	Ile	Asp	His	Asn	Ser	Val	Ser	His	Pro	Ser	Ala				
				470				475					480						
Asp	Phe	Phe	Gln	Ser	Cys	Gln	Lys	Met	Arg	Ser	Ile	Lys	Ala	Gly	Asp				
			485					490					495						
Asn	Pro	Phe	Gln	Cys	Thr	Cys	Glu	Leu	Arg	Glu	Phe	Val	Lys	Asn	Ile				
		500					505					510							
Asp	Gln	Val	Ser	Ser	Glu	Val	Leu	Glu	Gly	Trp	Pro	Asp	Ser	Tyr	Lys				

515	520	525
Cys Asp Tyr Pro Glu Ser Tyr Arg Gly Ser Pro Leu Lys Asp Phe His 530 535 540 545		
Met Ser Glu Leu Ser Cys Asn Ile Thr Leu Leu Ile Val Thr Ile Gly 550 555 560		
Ala Thr Met Leu Val Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr 565 570 575		
Leu Asp Leu Pro Trp Tyr Leu Arg Met Val Cys Gln Trp Thr Gln Thr 580 585 590		
Arg Arg Arg Ala Arg Asn Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu 595 600 605		
Gln Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Ala Trp Val 610 615 620 625		
Lys Ser Glu Leu Val Pro Tyr Leu Glu Lys Glu Asp Ile Gln Ile Cys 630 635 640		
Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile 645 650 655		
Ile Asn Cys Ile Glu Lys Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro 660 665 670		
Asn Phe Val Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His 675 680 685		
His Asn Leu Phe His Glu Gly Ser Asn Asn Leu Ile Leu Ile Leu Leu 690 695 700 705		
Glu Pro Ile Pro Gln Asn Ser Ile Pro Asn Lys Tyr His Lys Leu Lys 710 715 720		
Ala Leu Met Thr Gln Arg Thr Tyr Leu Gln Trp Pro Lys Glu Lys Ser 725 730 735		
Lys Arg Gly Leu Phe Trp Ala Asn Ile Arg Ala Ala Phe Asn Met Lys 740 745 750		
Leu Thr Leu Val Thr Glu Asn Asn Asp Val Lys Ser 755 760 765		

<210> 42  
 <211> 3168  
 <212> DNA  
 <213> Unknown

<220>  
<223> Description of Unknown Organism:primate; surmised  
Homo sapiens

<220>  
<221> CDS  
<222> (1)..(3165)

<220>  
<221> mat\_peptide  
<222> (144)..(3165)

<400> 42  
atg ccc atg aag tgg agt ggg tgg agg tgg agc tgg ggg ccg gcc act 48  
Met Pro Met Lys Trp Ser Gly Trp Arg Trp Ser Trp Gly Pro Ala Thr  
-45 -40 -35  
  
cac aca gcc ctc cca ccc cca cag ggt ttc tgc cgc agc gcc ctg cac 96  
His Thr Ala Leu Pro Pro Pro Gln Gly Phe Cys Arg Ser Ala Leu His  
-30 -25 -20  
  
ccg ctg tct ctc ctg gtg cag gcc atc atg ctg gcc atg acc ctg gcc 144  
Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu Ala  
-15 -10 -5 -1  
  
ctg ggt acc ttg cct gcc ttc cta ccc tgt gag ctc cag ccc cac ggc 192  
Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His Gly  
1 5 10 15  
  
ctg gtg aac tgc aac tgg ctg ttc ctg aag tct gtg ccc cac ttc tcc 240  
Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser  
20 25 30  
  
atg gca gca ccc cgt ggc aat gtc acc agc ctt tcc ttg tcc tcc aac 288  
Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn  
35 40 45  
  
cgc atc cac cac ctc cat gat tct gac ttt gcc cac ctg ccc agc ctg 336  
Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu  
50 55 60  
  
cgg cat ctc aac ctc aag tgg aac tgc ccg ccg gtt ggc ctc agc ccc 384  
Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro  
65 70 75 80  
  
atg cac ttc ccc tgc cac atg acc atc gag ccc agc acc ttc ttg gct 432  
Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala  
85 90 95  
  
gtg ccc acc ctg gaa gag cta aac ctg agc tac aac aac atc atg act 480  
Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr  
100 105 110  
  
gtg cct gcg ctg ccc aaa tcc ctc ata tcc ctg tcc ctc agc cat acc 528

Val	Pro	Ala	Leu	Pro	Lys	Ser	Leu	Ile	Ser	Leu	Ser	Leu	Ser	His	Thr		
		115					120					125					
aac	atc	ctg	atg	cta	gac	tct	gcc	agc	ctc	gcc	ggc	ctg	cat	gcc	ctg	576	
Asn	Ile	Leu	Met	Leu	Asp	Ser	Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu		
	130					135					140						
cgc	ttc	cta	ttc	atg	gac	ggc	aac	tgt	tat	tac	aag	aac	ccc	tgc	agg	624	
Arg	Phe	Leu	Phe	Met	Asp	Gly	Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg		
145					150					155					160		
cag	gca	ctg	gag	gtg	gcc	ccg	ggt	gcc	ctc	ctt	ggc	ctg	ggc	aac	ctc	672	
Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu		
				165					170					175			
acc	cac	ctg	tca	ctc	aag	tac	aac	aac	ctc	act	gtg	gtg	ccc	cgc	aac	720	
Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn		
			180					185					190				
ctg	ect	tcc	agc	ctg	gag	tat	ctg	ctg	ttg	tcc	tac	aac	cgc	atc	gtc	768	
Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val		
		195					200					205					
aaa	ctg	gcg	cct	gag	gac	ctg	gcc	aat	ctg	acc	gcc	ctg	cgt	gtg	ctc	816	
Lys	Leu	Ala	Pro	Glu	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu		
	210					215					220						
gat	gtg	ggc	gga	aat	tgc	cgc	cgc	tgc	gac	cac	gct	ccc	aac	ccc	tgc	864	
Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys		
225					230					235					240		
atg	gag	tgc	cct	cgt	cac	ttc	ccc	cag	cta	cat	ccc	gat	acc	ttc	agc	912	
Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser		
				245					250					255			
-cac	ctg	agc	cgt	ctt	gaa	ggc	ctg	gtg	ttg	aag	gac	agt	tct	ctc	tcc	960	
His	Leu	Ser	Arg	Leu	Glu	Gly	Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser		
			260					265					270				
tgg	ctg	aat	gcc	agt	tgg	ttc	cgt	ggg	ctg	gga	aac	ctc	cga	gtg	ctg	1008	
Trp	Leu	Asn	Ala	Ser	Trp	Phe	Arg	Gly	Leu	Gly	Asn	Leu	Arg	Val	Leu		
		275					280					285					
gac	ctg	agt	gag	aac	ttc	ctc	tac	aaa	tgc	atc	act	aaa	acc	aag	gcc	1056	
Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala		
	290					295					300						
ttc	cag	ggc	cta	aca	cag	ctg	cgc	aag	ctt	aac	ctg	tcc	ttc	aat	tac	1104	
Phe	Gln	Gly	Leu	Thr	Gln	Leu	Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr		
305					310					315					320		
caa	aag	agg	gtg	tcc	ttt	gcc	cac	ctg	tct	ctg	gcc	cct	tcc	ttc	ggg	1152	
Gln	Lys	Arg	Val	Ser	Phe	Ala	His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly		

325

330

335

1200

agc ctg gtc gcc ctg aag gag ctg gac atg cac ggc atc ttc ttc cgc  
 Ser Leu Val Ala Leu Lys Glu Leu Asp Met His Gly Ile Phe Phe Arg  
 340 345 350

1248

cca ctc gat gag acc acg ctc cgg cca ctg gcc cgc ctg ccc atg ctc  
 Ser Leu Asp Glu Thr Thr Leu Arg Pro Leu Ala Arg Leu Pro Met Leu  
 355 360 365

1296

cag act ctg cgt ctg cag atg aac ttc atc aac cag gcc cag ctc ggc  
 Gln Thr Leu Arg Leu Gln Met Asn Phe Ile Asn Gln Ala Gln Leu Gly  
 370 375 380

1344

atc ttc agg gcc ttc cct ggc ctg cgc tac gtg gac ctg tgc gac aac  
 Ile Phe Arg Ala Phe Pro Gly Leu Arg Tyr Val Asp Leu Ser Asp Asn  
 385 390 395 400

1392

cgc atc agc gga gct tgc gag ctg aca gcc acc atg ggg gag gca gat  
 Arg Ile Ser Gly Ala Ser Glu Leu Thr Ala Thr Met Gly Glu Ala Asp  
 405 410 415

1440

gga ggc gag aag gtc tgg ctg cag cct ggg gac ctt gct ccg gcc cca  
 Gly Gly Glu Lys Val Trp Leu Gln Pro Gly Asp Leu Ala Pro Ala Pro  
 420 425 430

1488

gtg gac act ccc agc tct gaa gac ttc agg ccc aac tgc agc acc ctc  
 Val Asp Thr Pro Ser Ser Glu Asp Phe Arg Pro Asn Cys Ser Thr Leu  
 435 440 445

1536

aac ttc acc ttg gat ctg tca cgg aac aac ctg gtg acc gtg cag ccg  
 Asn Phe Thr Leu Asp Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro  
 450 455 460

1584

gag atg ttt gcc cag ctc tgc cac ctg cag tgc ctg cgc ctg agc cac  
 Glu Met Phe Ala Gln Leu Ser His Leu Gln Cys Leu Arg Leu Ser His  
 465 470 475 480

1632

aac tgc atc tgc cag gca gtc aat ggc tcc cag ttc ctg ccg ctg acc  
 Asn Cys Ile Ser Gln Ala Val Asn Gly Ser Gln Phe Leu Pro Leu Thr  
 485 490 495

1680

ggt ctg cag gtg cta gac ctg tcc cac aat aag ctg gac ctc tac cac  
 Gly Leu Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His  
 500 505 510

1728

gag cac tca ttc acg gag cta cca cga ctg gag gcc ctg gac ctc agc  
 Glu His Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser  
 515 520 525

1776

tac aac agc cag ccc ttt ggc atg cag ggc gtg ggc cac aac ttc agc  
 Tyr Asn Ser Gln Pro Phe Gly Met Gln Gly Val Gly His Asn Phe Ser  
 530 535 540

ctc	gtg	gct	cac	ctg	cgc	acc	ctg	cgc	cac	ctc	agc	ctg	gcc	cac	aac	1824
Phe	Val	Ala	His	Leu	Arg	Thr	Leu	Arg	His	Leu	Ser	Leu	Ala	His	Asn	
545					550					555					560	
aac	atc	cac	agc	caa	gtg	tcc	cag	cag	ctc	tgc	agt	acg	tcg	ctg	cgg	1872
Asn	Ile	His	Ser	Gln	Val	Ser	Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Arg	
				565					570						575	
gcc	ctg	gac	ttc	agc	ggc	aat	gca	ctg	ggc	cat	atg	tgg	gcc	gag	gga	1920
Ala	Leu	Asp	Phe	Ser	Gly	Asn	Ala	Leu	Gly	His	Met	Trp	Ala	Glu	Gly	
			580					585					590			
gac	ctc	tat	ctg	cac	ttc	ttc	caa	ggc	ctg	agc	ggg	ttg	atc	tgg	ctg	1968
Asp	Leu	Tyr	Leu	His	Phe	Phe	Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	
		595					600					605				
gac	ttg	tcc	cag	aac	cgc	ctg	cac	acc	ctc	ctg	ccc	caa	acc	ctg	cgc	2016
Asp	Leu	Ser	Gln	Asn	Arg	Leu	His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	
	610					615					620					
aac	ctc	ccc	aag	agc	cta	cag	gtg	ctg	cgt	ctc	cgt	gac	aat	tac	ctg	2064
Asn	Leu	Pro	Lys	Ser	Leu	Gln	Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	
625					630				635						640	
gcc	ctc	ttt	aag	tgg	tgg	agc	ctc	cac	ttc	ctg	ccc	aaa	ctg	gaa	gtc	2112
Ala	Phe	Phe	Lys	Trp	Trp	Ser	Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	
				645					650					655		
ctc	gac	ctg	gca	gga	aac	cag	ctg	aag	gcc	ctg	acc	aat	ggc	agc	ctg	2160
Leu	Asp	Leu	Ala	Gly	Asn	Gln	Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	
			660					665					670			
cct	gct	ggc	acc	cgg	ctc	cgg	agg	ctg	gat	gtc	agc	tgc	aac	agc	atc	2208
Pro	Ala	Gly	Thr	Arg	Leu	Arg	Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	Ile	
		675					680					685				
agc	ttc	gtg	gcc	ccc	ggc	ttc	ttt	tcc	aag	gcc	aag	gag	ctg	cga	gag	2256
Ser	Phe	Val	Ala	Pro	Gly	Phe	Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	Glu	
						695					700					
ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	aca	gtg	gac	cac	tcc	tgg	ttt	2304
Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	Thr	Val	Asp	His	Ser	Trp	Phe	
					710					715					720	
ggg	ccc	ctg	gcg	agt	gcc	ctg	caa	ata	cta	gat	gta	agc	gcc	aac	cct	2352
Gly	Pro	Leu	Ala	Ser	Ala	Leu	Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	
				725					730					735		
ctg	cac	tgc	gcc	tgt	ggg	gcg	gcc	ttt	atg	gac	ttc	ctg	ctg	gag	gtg	2400
Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	
			740					745					750			
cag	gct	gcc	gtg	ccc	ggg	ctg	ccc	agc	cgg	gtg	aag	tgt	ggc	agt	ccg	2448



Gln	Ala	Ala	Val	Pro	Gly	Leu	Pro	Ser	Arg	Val	Lys	Cys	Gly	Ser	Pro		
	755						760					765					
ggc	cag	ctc	cag	ggc	ctc	agc	atc	ttt	gca	cag	gac	ctg	cgc	ctc	tgc	2496	
Gly	Gln	Leu	Gln	Gly	Leu	Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys		
	770					775					780						
ctg	gat	gag	gcc	ctc	tcc	tgg	gac	tgt	ttc	gcc	ctc	tgc	ctg	ctg	gct	2544	
Leu	Asp	Glu	Ala	Leu	Ser	Trp	Asp	Cys	Phe	Ala	Leu	Ser	Leu	Leu	Ala		
	785				790					795					800		
gtg	gct	ctg	ggc	ctg	ggg	gtg	ccc	atg	ctg	cat	cac	ctc	tgt	ggc	tgg	2592	
Val	Ala	Leu	Gly	Leu	Gly	Val	Pro	Met	Leu	His	His	Leu	Cys	Gly	Trp		
				805					810					815			
gac	ctc	tgg	tac	tgc	ttc	cac	ctg	tgc	ctg	gcc	tgg	ctt	ccc	tgg	cgg	2640	
Asp	Leu	Trp	Tyr	Cys	Phe	His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Trp	Arg		
			820					825					830				
ggg	cgg	caa	agt	ggg	cga	gat	gag	gat	gcc	ctg	ccc	tac	gat	gcc	ttc	2688	
Gly	Arg	Gln	Ser	Gly	Arg	Asp	Glu	Asp	Ala	Leu	Pro	Tyr	Asp	Ala	Phe		
	835						840					845					
gtg	gtc	ttc	gac	aaa	acg	cag	agc	gca	gtg	gca	gac	tgg	gtg	tac	aac	2736	
Val	Val	Phe	Asp	Lys	Thr	Gln	Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn		
	850					855					860						
gag	ttt	cgg	ggg	cag	ctg	gag	gag	tgc	cgt	ggg	cgc	tgg	gca	ctc	cgc	2784	
Glu	Leu	Arg	Gly	Gln	Leu	Glu	Glu	Cys	Arg	Gly	Arg	Trp	Ala	Leu	Arg		
	865				870					875					880		
ctg	tgc	ctg	gag	gaa	cgc	gac	tgg	ctg	cct	ggc	aaa	acc	ctc	ttt	gag	2832	
Leu	Cys	Leu	Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Lys	Thr	Leu	Phe	Glu		
				885					890					895			
aac	ctg	tgg	gcc	tgc	gtc	tat	ggc	agc	cgc	aag	acg	ctg	ttt	gtg	ctg	2880	
Asn	Leu	Trp	Ala	Ser	Val	Tyr	Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu		
			900					905					910				
gcc	cac	acg	gac	cgg	gtc	agt	ggg	ctc	ttg	cgc	gcc	agc	ttc	ctg	ctg	2928	
Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu	Arg	Ala	Ser	Phe	Leu	Leu		
			915				920					925					
gcc	cag	cag	cgc	ctg	ctg	gag	gac	cgc	aag	gac	gtc	gtg	gtg	ctg	gtg	2976	
Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val		
	930					935					940						
atc	ctg	agc	cct	gac	ggc	cgc	cgc	tcc	cgc	tat	gtg	cgg	ctg	cgc	cag	3024	
Ile	Leu	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln		
	945				950					955					960		
cgc	ctc	tgc	cgc	cag	agt	gtc	ctc	ctc	tgg	ccc	cac	cag	ccc	agt	ggg	3072	
Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Leu	Trp	Pro	His	Gln	Pro	Ser	Gly		
				965					970					975			

cag cgc agc ttc tgg gcc cag ctg ggc atg gcc ctg acc agg gac aac 3120  
 gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp Asn  
 980 985 990

cac cac ttc tat aac cgg aac ttc tgc cag gga ccc acg gcc gaa tag 3168  
 His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu  
 995 1000 1005

<210> 43  
 <211> 1055  
 <212> PRT  
 <213> Unknown

<400> 43  
 Met Pro Met Lys Trp Ser Gly Trp Arg Trp Ser Trp Gly Pro Ala Thr  
 -45 -40 -35

His Thr Ala Leu Pro Pro Pro Gln Gly Phe Cys Arg Ser Ala Leu His  
 -30 -25 -20

Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu Ala  
 15 -10 -5 -1

Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His Gly  
 1 5 10 15

Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser  
 20 25 30

Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn  
 35 40 45

Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu  
 50 55 60

Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro  
 65 70 75 80

Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala  
 85 90 95

Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr  
 100 105 110

Val Pro Ala Leu Pro Lys Ser Leu Ile Ser Leu Ser Leu Ser His Thr  
 115 120 125

Asn Ile Leu Met Leu Asp Ser Ala Ser Leu Ala Gly Leu His Ala Leu  
 130 135 140

Arg Phe Leu Phe Met Asp Gly Asn Cys Tyr Tyr Lys Asn Pro Cys Arg

145		150		155		160									
Gln	Ala	Leu	Glu	Val	Ala	Pro	Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu
				165					170					175	
Thr	His	Leu	Ser	Leu	Lys	Tyr	Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn
			180					185					190		
Leu	Pro	Ser	Ser	Leu	Glu	Tyr	Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val
		195					200					205			
Lys	Leu	Ala	Pro	Glu	Asp	Leu	Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu
		210				215					220				
Asp	Val	Gly	Gly	Asn	Cys	Arg	Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys
225					230					235					240
Met	Glu	Cys	Pro	Arg	His	Phe	Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser
				245					250					255	
His	Leu	Ser	Arg	Leu	Glu	Gly	Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser
			260					265					270		
Trp	Leu	Asn	Ala	Ser	Trp	Phe	Arg	Gly	Leu	Gly	Asn	Leu	Arg	Val	Leu
		275					280					285			
Asp	Leu	Ser	Glu	Asn	Phe	Leu	Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala
		290				295					300				
Phe	Gln	Gly	Leu	Thr	Gln	Leu	Arg	Lys	Leu	Asn	Leu	Ser	Phe	Asn	Tyr
305					310					315					320
Gln	Lys	Arg	Val	Ser	Phe	Ala	His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly
				325					330					335	
Ser	Leu	Val	Ala	Leu	Lys	Glu	Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg
			340					345					350		
Ser	Leu	Asp	Glu	Thr	Thr	Leu	Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu
		355					360					365			
Gln	Thr	Leu	Arg	Leu	Gln	Met	Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly
		370				375					380				
Ile	Phe	Arg	Ala	Phe	Pro	Gly	Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn
385					390					395					400
Arg	Ile	Ser	Gly	Ala	Ser	Glu	Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp
				405					410					415	
Gly	Gly	Glu	Lys	Val	Trp	Leu	Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro
			420					425					430		
Val	Asp	Thr	Pro	Ser	Ser	Glu	Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu

435

440

445

Asn Phe Thr Leu Asp Leu Ser Arg Asn Asn Leu Val Thr Val Gln Pro  
 450 455 460

Glu Met Phe Ala Gln Leu Ser His Leu Gln Cys Leu Arg Leu Ser His  
 465 470 475 480

Asn Cys Ile Ser Gln Ala Val Asn Gly Ser Gln Phe Leu Pro Leu Thr  
 485 490 495

Gly Leu Gln Val Leu Asp Leu Ser His Asn Lys Leu Asp Leu Tyr His  
 500 505 510

Glu His Ser Phe Thr Glu Leu Pro Arg Leu Glu Ala Leu Asp Leu Ser  
 515 520 525

Tyr Asn Ser Gln Pro Phe Gly Met Gln Gly Val Gly His Asn Phe Ser  
 530 535 540

Phe Val Ala His Leu Arg Thr Leu Arg His Leu Ser Leu Ala His Asn  
 545 550 555 560

Asn Ile His Ser Gln Val Ser Gln Gln Leu Cys Ser Thr Ser Leu Arg  
 565 570 575

Ala Leu Asp Phe Ser Gly Asn Ala Leu Gly His Met Trp Ala Glu Gly  
 580 585 590

Asp Leu Tyr Leu His Phe Phe Gln Gly Leu Ser Gly Leu Ile Trp Leu  
 595 600 605

Asp Leu Ser Gln Asn Arg Leu His Thr Leu Leu Pro Gln Thr Leu Arg  
 610 615 620

Asn Leu Pro Lys Ser Leu Gln Val Leu Arg Leu Arg Asp Asn Tyr Leu  
 625 630 635 640

Ala Phe Phe Lys Trp Trp Ser Leu His Phe Leu Pro Lys Leu Glu Val  
 645 650 655

Leu Asp Leu Ala Gly Asn Gln Leu Lys Ala Leu Thr Asn Gly Ser Leu  
 660 665 670

Pro Ala Gly Thr Arg Leu Arg Arg Leu Asp Val Ser Cys Asn Ser Ile  
 675 680 685

Ser Phe Val Ala Pro Gly Phe Phe Ser Lys Ala Lys Glu Leu Arg Glu  
 690 695 700

Leu Asn Leu Ser Ala Asn Ala Leu Lys Thr Val Asp His Ser Trp Phe  
 705 710 715 720

Gly Pro Leu Ala Ser Ala Leu Gln Ile Leu Asp Val Ser Ala Asn Pro  
725 730 735

Leu His Cys Ala Cys Gly Ala Ala Phe Met Asp Phe Leu Leu Glu Val  
740 745 750

Gln Ala Ala Val Pro Gly Leu Pro Ser Arg Val Lys Cys Gly Ser Pro  
755 760 765

Gly Gln Leu Gln Gly Leu Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys  
770 775 780

Leu Asp Glu Ala Leu Ser Trp Asp Cys Phe Ala Leu Ser Leu Leu Ala  
785 790 795 800

Val Ala Leu Gly Leu Gly Val Pro Met Leu His His Leu Cys Gly Trp  
805 810 815

Asp Leu Trp Tyr Cys Phe His Leu Cys Leu Ala Trp Leu Pro Trp Arg  
820 825 830

Gly Arg Gln Ser Gly Arg Asp Glu Asp Ala Leu Pro Tyr Asp Ala Phe  
835 840 845

Val Val Phe Asp Lys Thr Gln Ser Ala Val Ala Asp Trp Val Tyr Asn  
850 855 860

Glu Leu Arg Gly Gln Leu Glu Glu Cys Arg Gly Arg Trp Ala Leu Arg  
865 870 875 880

Leu Cys Leu Glu Glu Arg Asp Trp Leu Pro Gly Lys Thr Leu Phe Glu  
885 890 895

Asn Leu Trp Ala Ser Val Tyr Gly Ser Arg Lys Thr Leu Phe Val Leu  
900 905 910

Ala His Thr Asp Arg Val Ser Gly Leu Leu Arg Ala Ser Phe Leu Leu  
915 920 925

Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys Asp Val Val Val Leu Val  
930 935 940

Ile Leu Ser Pro Asp Gly Arg Arg Ser Arg Tyr Val Arg Leu Arg Gln  
945 950 955 960

Arg Leu Cys Arg Gln Ser Val Leu Leu Trp Pro His Gln Pro Ser Gly  
965 970 975

Gln Arg Ser Phe Trp Ala Gln Leu Gly Met Ala Leu Thr Arg Asp Asn  
980 985 990

His His Phe Tyr Asn Arg Asn Phe Cys Gln Gly Pro Thr Ala Glu  
995 1000 1005

<210> 44  
<211> 2289  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism:rodent; surmised  
Mus musculus

<220>  
<221> CDS  
<222> (1)..(2079)

<400> 44  
aac ctg tcc ttc aat tac cgc aag aag gta tcc ttt gcc cgc ctc cac 48  
Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala Arg Leu His  
1 5 10 15  
ctg gca agt tcc ttt aag aac ctg gtg tca ctg cag gag ctg aac atg 96  
Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met  
20 25 30  
aac ggc atc ttc ttc cgc ttg ctc aac aag tac acg ctc aga tgg ctg 144  
Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu  
35 40 45  
gcc gat ctg ccc aaa ctc cac act ctg cat ctt caa atg aac ttc atc 192  
Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile  
50 55 60  
aac cag gca cag ctc agc atc ttt ggt acc ttc cga gcc ctt cgc ttt 240  
Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe  
65 70 75 80  
gtg gac ttg tca gac aat cgc atc agt ggg cct tca acg ctg tca gaa 288  
Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu  
85 90 95  
gcc acc cct gaa gag gca gat gat gca gag cag gag gag ctg ttg tct 336  
Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser  
100 105 110  
gcg gat cct cac cca gct ccg ctg agc acc cct gct tct aag aac ttc 384  
Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe  
115 120 125  
atg gac agg tgt aag aac ttc aag ttc aac atg gac ctg tct cgg aac 432  
Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn  
130 135 140  
aac ctg gtg act atc aca gca gag atg ttt gta aat ctc tca cgc ctc 480  
Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu

145	150	155	160	
cag tgt ctt agc ctg agc cac aac tca att gca cag gct gtc aat ggc				528
Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala Val Asn Gly	165	170	175	
tct cag ttc ctg ccg ctg acc ggt ctg cag gtg cta gac ctg tcc cac				576
Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His	180	185	190	
aat aag ctg gac ctc tac cac gag cac tca ttc acg gag cta cca cga				624
Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu Pro Arg	195	200	205	
ctg gag gcc ctg gac ctc agc tac aac agc cag ccc ttt agc atg aag				672
Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys	210	215	220	
ggt ata ggc cac aat ttc agt ttt gtg acc cat ctg tcc atg cta cag				720
Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser Met Leu Gln	225	230	235	240
agc ctt agc ctg gca cac aat gac att cat acc cgt gtg tcc tca cat				768
Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val Ser Ser His	245	250	255	
ctc aac agc aac tca gtg agg ttt ctt gac ttc agc ggc aac ggt atg				816
Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly Asn Gly Met	260	265	270	
ggc cgc atg tgg gat gag ggg ggc ctt tat ctc cat ttc ttc caa ggc				864
Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe Phe Gln Gly	275	280	285	
ctg agt ggc gtg ctg aag ctg gac ctg tct caa aat aac ctg cat atc				912
Leu Ser Gly Val Leu Lys Leu Asp Leu Ser Gln Asn Asn Leu His Ile	290	295	300	
ctc cgg ccc cag aac ctt gac aac ctc ccc aag agc ctg aag ctg ctg				960
Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu Lys Leu Leu	305	310	315	320
agc ctc cga gac aac tac cta tct ttc ttt aac tgg acc agt ctg tcc				1008
Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr Ser Leu Ser	325	330	335	
ttc cta ccc aac ctg gaa gtc cta gac ctg gca ggc aac cag cta aag				1056
Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys	340	345	350	
gcc ctg acc aat ggc acc ctg cct aat ggc acc ctc ctc cag aaa ctc				1104
Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu Gln Lys Leu	355	360	365	

gat	gtc	agt	agc	aac	agt	atc	gtc	tct	gtg	gcc	ccc	ggc	ttc	ttt	tcc	1152
Asp	Val	Ser	Ser	Asn	Ser	Ile	Val	Ser	Val	Ala	Pro	Gly	Phe	Phe	Ser	
370						375					380					
aag	gcc	aag	gag	ctg	cga	gag	ctc	aac	ctt	agc	gcc	aac	gcc	ctc	aag	1200
Lys	Ala	Lys	Glu	Leu	Arg	Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala	Leu	Lys	
385					390					395					400	
aca	gtg	gac	cac	tcc	tgg	ttt	ggg	ccc	att	gtg	atg	aac	ctg	aca	gtt	1248
Thr	Val	Asp	His	Ser	Trp	Phe	Gly	Pro	Ile	Val	Met	Asn	Leu	Thr	Val	
				405					410					415		
cta	gac	gtg	aga	agc	aac	cct	ctg	cac	tgt	gcc	tgt	ggg	gca	gcc	ttc	1296
Leu	Asp	Val	Arg	Ser	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly	Ala	Ala	Phe	
			420					425					430			
gta	gac	tta	ctg	ttg	gag	gtg	cag	acc	aag	gtg	cct	ggc	ctg	gct	aat	1344
Val	Asp	Leu	Leu	Leu	Glu	Val	Gln	Thr	Lys	Val	Pro	Gly	Leu	Ala	Asn	
		435					440					445				
ggt	gtg	aag	tgt	ggc	agc	ccc	ggc	cag	ctg	cag	ggc	cgt	agc	atc	ttc	1392
Gly	Val	Lys	Cys	Gly	Ser	Pro	Gly	Gln	Leu	Gln	Gly	Arg	Ser	Ile	Phe	
	450					455					460					
gcg	cag	gac	ctg	cgg	ctg	tgc	ctg	gat	gag	gtc	ctc	tct	tgg	gac	tgc	1440
Ala	Gln	Asp	Leu	Arg	Leu	Cys	Leu	Asp	Glu	Val	Leu	Ser	Trp	Asp	Cys	
465					470					475					480	
ttt	ggc	ctt	tca	ctc	ttg	gct	gtg	gcc	gtg	ggc	atg	gtg	gtg	cct	ata	1488
Phe	Gly	Leu	Ser	Leu	Leu	Ala	Val	Ala	Val	Gly	Met	Val	Val	Pro	Ile	
				485					490					495		
ctg	cac	cat	ctc	tgc	ggc	tgg	gac	gtc	tgg	tac	tgt	ttt	cat	ctg	tgc	1536
Leu	His	His	Leu	Cys	Gly	Trp	Asp	Val	Trp	Tyr	Cys	Phe	His	Leu	Cys	
			500					505					510			
ctg	gca	tgg	cta	cct	ttg	cta	gcc	cgc	agc	cga	cgc	agc	gcc	caa	act	1584
Leu	Ala	Trp	Leu	Pro	Leu	Leu	Ala	Arg	Ser	Arg	Arg	Ser	Ala	Gln	Thr	
		515					520					525				
ctc	cct	tat	gat	gcc	ttc	gtg	gtg	ttc	gat	aag	gca	cag	agc	gca	gtt	1632
Leu	Pro	Tyr	Asp	Ala	Phe	Val	Val	Phe	Asp	Lys	Ala	Gln	Ser	Ala	Val	
	530					535					540					
gcc	gac	tgg	gtg	tat	aac	gag	ctg	cgg	gtg	cgg	ctg	gag	gag	cgg	cgc	1680
Ala	Asp	Trp	Val	Tyr	Asn	Glu	Leu	Arg	Val	Arg	Leu	Glu	Glu	Arg	Arg	
545					550					555					560	
ggc	cgc	tgg	gca	ctc	cgc	ctg	tgc	ctg	gag	gac	cga	gat	tgg	ctg	cct	1728
Gly	Arg	Trp	Ala	Leu	Arg	Leu	Cys	Leu	Glu	Asp	Arg	Asp	Trp	Leu	Pro	
				565				570						575		
ggc	cag	acg	ctc	ttc	gag	aac	ctc	tgg	gct	tcc	atc	tat	ggg	agc	cgc	1776



Gly	Gln	Thr	Leu	Phe	Glu	Asn	Leu	Trp	Ala	Ser	Ile	Tyr	Gly	Ser	Arg		
			580					585					590				
aag	act	cta	ttt	gtg	ctg	gcc	cac	acg	gac	cgc	gtc	agt	ggc	ctc	ctg	1824	
Lys	Thr	Leu	Phe	Val	Leu	Ala	His	Thr	Asp	Arg	Val	Ser	Gly	Leu	Leu		
		595					600					605					
cgc	acc	agc	ttc	ctg	ctg	gct	cag	cag	cgc	ctg	ttg	gaa	gac	cgc	aag	1872	
Arg	Thr	Ser	Phe	Leu	Leu	Ala	Gln	Gln	Arg	Leu	Leu	Glu	Asp	Arg	Lys		
		610				615					620						
gac	gtg	gtg	gtg	ttg	gtg	atc	ctg	cgt	ccg	gat	gcc	cac	cgc	tcc	cgc	1920	
Asp	Val	Val	Val	Leu	Val	Ile	Leu	Arg	Pro	Asp	Ala	His	Arg	Ser	Arg		
					630					635					640		
tat	gtg	cga	ctg	cgc	cag	cgt	ctc	tgc	cgc	cag	agt	gtg	ctc	ttc	tgg	1968	
Tyr	Val	Arg	Leu	Arg	Gln	Arg	Leu	Cys	Arg	Gln	Ser	Val	Leu	Phe	Trp		
				645					650					655			
ccc	cag	cag	ccc	aac	ggg	cag	ggg	ggc	ttc	tgg	gcc	cag	ctg	agt	aca	2016	
Pro	Gln	Gln	Pro	Asn	Gly	Gln	Gly	Gly	Phe	Trp	Ala	Gln	Leu	Ser	Thr		
			660					665					670				
gcc	ctg	act	agg	gac	aac	cgc	cac	ttc	tat	aac	cag	aac	ttc	tgc	cgg	2064	
Ala	Leu	Thr	Arg	Asp	Asn	Arg	His	Phe	Tyr	Asn	Gln	Asn	Phe	Cys	Arg		
		675					680					685					
gga	cct	aca	gca	gaa	tag	ctcagag	caacagctgg	aaacagctgc	atcttcatgt							2119	
Gly	Pro	Thr	Ala	Glu													
ctg	tttccc	agttgctctg	cctgccttgc	tctgtcttac	tacaccgcta	tttggcaagt										2179	
gcg	caatata	tgctaccaag	ccaccaggcc	cacggagcaa	aggttggctg	taaagggtag										2239	
ttttcttccc	atgcattctt	caggagagt	aagatagaca	ccaaacccac												2289	

<210> 45  
 <211> 693  
 <212> PRT  
 <213> Unknown

<400> 45  
 Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala Arg Leu His  
 1 5 10 15  
 Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu Leu Asn Met  
 20 25 30  
 Asn Gly Ile Phe Phe Arg Leu Leu Asn Lys Tyr Thr Leu Arg Trp Leu  
 35 40 45  
 Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met Asn Phe Ile

50

55

60

Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala Leu Arg Phe  
65 70 75 80

Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr Leu Ser Glu  
85 90 95

Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu Leu Leu Ser  
100 105 110

Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser Lys Asn Phe  
115 120 125

Met Asp Arg Cys Lys Asn Phe Lys Phe Asn Met Asp Leu Ser Arg Asn  
130 135 140

Asn Leu Val Thr Ile Thr Ala Glu Met Phe Val Asn Leu Ser Arg Leu  
145 150 155 160

Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala Val Asn Gly  
165 170 175

Ser Gln Phe Leu Pro Leu Thr Gly Leu Gln Val Leu Asp Leu Ser His  
180 185 190

Asn Lys Leu Asp Leu Tyr His Glu His Ser Phe Thr Glu Leu Pro Arg  
195 200 205

Leu Glu Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe Ser Met Lys  
210 215 220

Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser Met Leu Gln  
225 230 235 240

Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val Ser Ser His  
245 250 255

Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly Asn Gly Met  
260 265 270

Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe Phe Gln Gly  
275 280 285

Leu Ser Gly Val Leu Lys Leu Asp Leu Ser Gln Asn Asn Leu His Ile  
290 295 300

Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu Lys Leu Leu  
305 310 315 320

Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr Ser Leu Ser  
325 330 335

Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn Gln Leu Lys  
 340 345 350  
 Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu Gln Lys Leu  
 355 360 365  
 Asp Val Ser Ser Asn Ser Ile Val Ser Val Ala Pro Gly Phe Phe Ser  
 370 375 380  
 Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala Leu Lys  
 385 390 395 400  
 Thr Val Asp His Ser Trp Phe Gly Pro Ile Val Met Asn Leu Thr Val  
 405 410 415  
 Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly Ala Ala Phe  
 420 425 430  
 Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly Leu Ala Asn  
 435 440 445  
 Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg Ser Ile Phe  
 450 455 460  
 Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser Trp Asp Cys  
 465 470 475 480  
 Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val Val Pro Ile  
 485 490 495  
 Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe His Leu Cys  
 500 505 510  
 Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser Ala Gln Thr  
 515 520 525  
 Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln Ser Ala Val  
 530 535 540  
 Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu Glu Arg Arg  
 545 550 555 560  
 Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp Trp Leu Pro  
 565 570 575  
 Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr Gly Ser Arg  
 580 585 590  
 Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser Gly Leu Leu  
 595 600 605  
 Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu Asp Arg Lys  
 610 615 620

Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His Arg Ser Arg  
525 630 635 640

Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val Leu Phe Trp  
645 650 655

Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln Leu Ser Thr  
660 665 670

Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln Asn Phe Cys Arg  
675 680 685

Gly Pro Thr Ala Glu  
690

09550041-091001